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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

Run on:

June 9, 2005, 15:27:47; Search time 583 Seconds
(without alignments)
2275.470 Million cell updates/sec
Title:

US-10-812-620-2

Perfect score: 1179
Sequence:
1 MNSTKSPASHHTERGCFKNS......IPCFYSMPWICEMPEISPLD 214

Scoring table: BLOSUM6.2

Xgapop 10.0, Xgapext 0.5
Fgapop 10.0, Ygapext 7.0
Fgapop 0.0, Pgapext 7.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 6046767 segs, 3099530249 residues
Total number of hits satisfying chosen parameters: 12093534
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Minimum DB seq length: 0 Maximum DB seq length: 200000000 Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•			SUPERMITES			
Result	1	Query	1					
ON	score	Match	gth	g ;		Description		:
	1149		2517	21	US-10-812-62	Sequence	, r	Appli
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11	7	S.	997	10	-09-903-640-37	Sequence	376	App
12	7	S)	997	10	-09-908-093-37	Seguence	376	Api
13	~ 1	S L	997	200	-09-906-742-37	Sequence	376	Api
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18	٠.	S LO	997	2 2	-09-909-204-37	Seguence	376	Ap
19	2	S	997	10	-09-904-820-37	Sequence	376	Ap
50	7	S	997	9	-09-904-786-37	Sequence	376	Api
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33	-	S	997	10	-09-902-692-37	Seguence	376	Ap
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38	. ~	'n	997	ដ	-09-905-381-37	Sequence	3,	App
39	7	ß	997	2	-09-904-485-37	Sequence	37	Ap
40	2	S	997	2	-09-905-348-37	Seguence	5	Ap
41	~ [s c	997	2:	-09-905-088-37	Sequence	5	A P
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					ALIGNMENTS			
RESULT 1								
US-10-81	.2-620-1	pplicat	ion US,	/1081	2620			
, Public	ation	o. US20	0020019	360A1				
; GENEKAL INFORMATION: ; APPLICANT: Japan Science and	CANT	apan Sc	ience e		echnology Corporation			
FILE	REFEREN	CE: JAG	: A novel	·	ectin and			
CURRE	INT APPL	ICATION	NUMBE	D	8/10/812,620			
; CURRE	APPLIC	ATION N	S: ZOU4	-03- US/1	N 0			
; PRIOR	APPLIC	DATE:	2002-04 WWBER:	マ	11-293724			
PRIOR	FILING	DATE:	1999-10	Ŋ				
SEO ID 1	NO 1	2						

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| CAAATGTTCTTATGGACTGTTGCTGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATC 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731 USA
CURRENT PAPLICATION NUMBER: US/09/965,529
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL PROGRAM
SEQ ID NO 40
LENGTH: 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:

NAME KEY: misc feature

OTHER INFORMATION: Incyte ID No. US20020182671A1 1521513CB1
US-09-965-529-40
                                                                                                                                                                                              968
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Matches:
Conservative:
Mismatches:
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774.00
79.07%
66.51%
65.65%
                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-969-680A-40
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209
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                                                                Length:
Matches:
Conservative:
Mismatches:
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Publication No. US20020182671A1
GENERAL INFORMATION:
APPLICANT: YUE, Henry
APPLICANT: YUE, Henry
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, AMIA
APPLICANT: BANDMAN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: LU, Dyung Aina M.
APPLICANT: LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
                                                              1.4e-135
1149.00
98.13%
97.66%
                                                                                     Percent Similarity:
Best Local Similarity:
 LENGTH: 2517
TYPE: DNA
ORGANISM: Mouse
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US-09-965-529-40
                                                      Alignment Scores Pred. No.:
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180 AlaThrileArgAspSerSerAsnSerArgLysAsnTrpAsnAspileProCysPheTyr 199
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                  200 SerMetProTrpileCysGluMetProGluIleSerProLeuAsp 214
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FILE REFERENCE: 10466-14

CURRENT PELICATION NUMBER: US/09/909,320

CURRENT FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: US/09/04114

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-06

PRIOR FILING DATE: 1999-07-06

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-08

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/21647

PRIOR APPLICATION NUMBER: PCT/US99/21647

PRIOR APPLICATION NUMBER: PCT/US99/21647

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/28565
FILLING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                   Sequence 376, Application US/09909320 Patent No. US20020132240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Godowski, Paul J.
Grimaldi, Christopher J.
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Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Eaton, Dan L.
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219 CAAATGTICTTAIGGACIGTIGCIGGGAICCCCAICCTAITICTCAGIGCCIGTITCAIC 278
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OTHER INFORMATION: Incyte ID No. US20030124649A1 1521513CB1
                                                               APPLICANT: LAL, Preeti, YUE, Henry
APPLICANT: LAL, Preeti, YUE, Henry
APPLICANT: LAL, Preeti, YUE, Henry
APPLICANT: BURFOND, Neil; AZIMZAI, Yalda
APPLICANT: BURFOND, Neil; AZIMZAI, Yalda
APPLICANT: BATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731-1 USA
CURRENT APPLICATION NUMBER: US/09/969, 680A
CURRENT FILING DATE: 2001-10-02
PRIOR PILING DATE: 100-02
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/164,203
PRIOR APPLICATION NUMBER: 60/164,203
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 74
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Matches:
Conservative:
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Sequence 40, Application US/09969680A Publication No. US20030124649A1 GENERAL INFORMATION:
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774.00
79.07$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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LENGTH: 968
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774.00
Ashkenazi, Avi
Botstein, David
                              Desnoyers, Luc
Eaton, Dan L.
                                                                                      Fong, Sherman
Gao, Wei-Qiang
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US-09-909-088B-376
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Pred. No.:
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Mismatches:
Indels:
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Matches:
         PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PELING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 376
LENGTH: 997
PRIOR APPLICATION NUMBER: PCT/US99/30911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 376, Application US/0990908BB Patent No. US20020146709A1 GENERAL INFORMATION: APPLICANT: Genentech, Inc.
                                                                                                                                                                                                   2.95e-88
774.00
79.07%
66.51%
65.65%
                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-909-320-376
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Query Match:
                                                                                                                                                                                                                                   Percent Similarity:
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US-09-909-088B-376
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APPLICANT: Boneseth, David
APPLICANT: Boneseth, David
APPLICANT: Boneseth, David
APPLICANT: Bacon, Dan L.
APPLICANT: Reacon, Dan L.
APPLICANT: Garbier Blanch
APPLICANT: Garbier Blanch
APPLICANT: Goodeard, Am J.
APPLICANT: Grandled, Circleson, Manchel, J.
APPLICANT: Williams, J. Mickey
APPLICANT: Williams, J. Mickey
APPLICANT: Williams, J. Mickey
APPLICANT: Williams, J. Mickey
APPLICANT: Manchel, J.
APPLICANT: Williams, J. Mickey
APPLICANT: Manchel, J.
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                                                                                                             APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Tinothy A.
APPLICANT: Stewart, Tinothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/905,291A
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PRIOR PELICATION NUMBER: PCT/USO0/04114
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1090-07-06
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-09-08
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PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-03
PRIOR PLING DATE: 1000-01-05
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                                                                               Paoni, Nicholas F.
               Mather, Jennie P.
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       Conservative:
Mismatches:
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Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botsetein, David
APPLICANT: Besnoyers, Luc.
APPLICANT: Besnoyers, Luc.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Fivaroff, Ellen
APPLICANT: Fivaroff, Ellen
APPLICANT: Gao, Wei-Olang
APPLICANT: Gerber, Hangpeter
APPLICANT: Gecher, Hangpeter
APPLICANT: Goddard, A.
APPLICANT: Goddard, A.
APPLICANT: Goddard, A.
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kennech, J.
Kljavin, Ivar J.
   79.07%
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65.65%
Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-905-291A-376
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ORGANISM: Homo Sapien
US-09-902-853-376
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Best Local Similarity:
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120 ThrGlnGluGluGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
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                                                                                                                                                                                                                                                                                     180 AlaThrileArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
                                                                                                                                                                                                                                                                                                                                                                                                643 GCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGAATGATGTAACCTGTTTCCTC 702
                                                                                                  CysProleuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
                                    60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys
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CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 376, Application US/09902853
Publication No. US2002012659A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bothemazi, Avi
APPLICANT: Bothemazi, Avi
APPLICANT: Betsein, David
APPLICANT: Eaton, Dan L
APPLICANT: Fairara, Napoleone
APPLICANT: Frarara, Napoleone
APPLICANT: Forgy, Sherman
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Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Rijavin, Jame P.
Pan, James
Paoni, Nicholas F.
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APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Towart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and T
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Gerritsen, Mary E.
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US-09-902-853-376
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
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                                                     GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, Daniel
APPLICANT: William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-03-22
PRIOR PELICATION NUMBER: PCT/US00/04114
PRIOR PLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PRIOR DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
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APPLICANT: Ashkenari, Avi
APPLICANT: Botsein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR FILING DATE: 1999-12-20
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                                                                                               MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
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                                                         US-10-812-620-2 (1-214) x US-09-907-841-376 (1-997)
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
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Mather, Jennie P
Pan, James
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Gao, Wei-Qiang
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APPLICANT: Stewart, Timethy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, I.
APPLICANT: William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907, 841
CURRENT PILING DATE: 2000-02-22
PRIOR PRILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
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SEQ ID NO 376
LENGTH: 997
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Matches:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Roy, Margaret Ann
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Hillan, Kenneth,
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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US-09-907-841-376
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Best Local Similarity:
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                                                                                                                                                                                              TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-11 CURRENT APPLICATION NUMBER: US/09/903,640 CURRENT FILING DATE: 2001-07-11 PRIOR APPLICATION NUMBER: 09/665,350 PRIOR PILING DATE: 2000-09-18 NUMBER OF SEQ ID NOS: 423
                                                                                                 CCTGAGAATTTCACAGAGCTCTCCTGCTACAATTATGGATCAGGTTCAGTCAAGAATTGT
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Godowski, Paul J.
Grimaldi, Christopher J.
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Kljavin, Ivar J.
Mather, Jennie P.
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Gerritsen, Mary E.
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Roy, Margaret Ann
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Gao, Wei-Qiang
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                                                                         APPLICAWY: Williams, Daniel
APPLICAWY: Williams, Daniel
APPLICAWY: Williams, Daniel
APPLICAWY: Williams, Dinkey
APPLICAWY: Wood, William, I
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 1006-07-11
CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT APPLICATION NUMBER: US/09/904.011
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-27
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US99/28014
PRIOR PELING DATE: 1999-10-10
PRIOR APPLICATION NUMBER: PCT/US99/28014
PRIOR PELING DATE: 1999-11-00
PRIOR APPLICATION NUMBER: PCT/US99/28054
PRIOR PELING DATE: 1999-11-00
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28056
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-07
PRIOR P
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Indels:
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                     Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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US-09-904-011-376
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Best Local Similarity:
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritean, Mary E.
Goddward, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Grimaldi, Christopher J.
Kljavin, Ivar J.
Mather, Jennie P.
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ORGANISM: Homo Sapien
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
                                                                                                                                                                                                                                           GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
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                                                                                                                                                                                            1 MetAsinSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsinSer 20
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Mismatches:
Indels:
Gaps:
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                                                                                     Length:
Matches:
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Publication No. US20030017498A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botherazi, Avi
APPLICANT: Botherazi, David
APPLICANT: Betsein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Fatoraza, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Forg, Sherman
                                                                                2.95e-88
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                          ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-640-376
                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-908-093-376
                                                                       Alignment Scores:
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 SEQ ID NO 376
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Mismatches:
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APPLICANT: Williams, Dannel, I.T. TITLE OF INVENTION: Acids Encoding the Same CIRRENT APPLICANTION NUMBER: US/09/906,742
CURRENT PILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/66,350
PRIOR FILING DATE: 2000-03-201
PRIOR APPLICATION NUMBER: 06/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR PAPLICATION NUMBER: PCT/US99/28014
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/20095
PRIOR APPLICATION NUMBER: PCT/US99/20095
PRIOR APPLICATION NUMBER: PCT/US99/20095
PRIOR APPLICATION NUMBER: PCT/US99/20099
PRIOR APPLICATION NUMBER: PCT/US99/20091
PRIOR APPLICATION NUMBER: PCT/US99/20099
PRIOR PELING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/20099
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DAT
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Mismatches:
Indels:
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Best Local Similarity:
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US-09-906-742-376
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DB:
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                                                                                                                            GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPhelle 40
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                                                                                                                                                                                                                                                                                                     60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
                                                                                                                                                                                                                                                                                                                                                                                           CysProleuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
                                      200 SerMetProTrplleCysGluMetProGluIleSerProLeuAsp 214
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AATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTGAAC 747
US-10-812-620-2 (1-214) x US-09-908-093-376 (1-997)
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Godowski, Paul J.
Gotimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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; Sequence 376, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORWATION:
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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APPLICANT: Abhkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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ThrGlnGluGluGluGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PLLING DATE: 1999-07-26
PRIOR PLLING DATE: 1999-07-28
PRIOR PLLING DATE: 1999-07-28
PRIOR PLLING DATE: 1999-09-08
PRIOR PLLING DATE: 1999-09-08
PRIOR PLLING DATE: 1999-09-08
PRIOR PLLING DATE: 1999-09-13
PRIOR PLLING DATE: 1999-09-15
PRIOR PLLING DATE: 1999-11-29
PRIOR PLLING DATE: 1999-11-29
PRIOR PLLING DATE: 1999-11-30
PRIOR PLLING DATE: 1999-11-30
PRIOR PLLING DATE: 1999-11-30
PRIOR PLLING DATE: 1999-12-02
PRIOR PLLING DATE: 1999-12-03
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SEQ ID NO 376
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Best Local Similarity:
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APPLICANT: Goddard, Paul J.
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Mather, Jennie P.
APPLICANT: Paon, Vames
APPLICANT: Paon, Nicholas F.
APPLICANT: Paon, Nicholas F.
APPLICANT: Stewart, Tinothy A.
APPLICANT: Vumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, P. Arickey
APPLICANT: William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
                                                342
                                                                                     GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
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                                283 CCTGAGAATTTCACAGAGCTCTCCTGCTACAATTATGGAICAGGTTCAGTCAAGAATTGT
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CURRENT APPLICATION NUMBER: 2001-07-16
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILING DATE: 2000-02-18
PRIOR PLING DATE: 2000-02-22
PRIOR PLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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Publication No. US20030027143A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Gerritsen, Mary E
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APPLICANT: Pan, Nicholas F.
APPLICANT: Stewart, Timochy A.
APPLICANT: Stewart, Timochy A.
APPLICANT: Stewart, Timochy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Screted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US 60/1414
FRIOR APPLICATION NUMBER: US 60/145,698
FRIOR PILING DATE: 1999-07-26
FRIOR PILING DATE: 1999-07-26
FRIOR FILING DATE: 1999-07-26
FRIOR PILING DATE: 1999-09-08
FRIOR FILING DATE: 1999-09-08
FRIOR FILING DATE: 1999-09-08
FRIOR FILING DATE: 1999-09-03
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FRIOR FILING DATE: 1999-09-03
FRIOR FILING DATE: 1999-09-03
FRIOR FILING DATE: 1999-09-15
FRIOR PILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
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                                TCACAGGAGGAGGAATTCCTTTCCTACAAGAAACCTAAAATGAGAGAGTTTTTATT
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Publication No. US20030027145A1
GENERAL INFORMATION:
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
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Paoni, Nicholas F.
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Gerber, Hanspeter
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
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|CAAATGTTCTTATGGACTGTTGCTGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATC 222
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Mismatches:
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Matches:
PRIOR APPLICATION NUMBER: PCI/US99/28319
PRIOR APPLICATION NUMBER: PCI/US99/28564
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-16
PRIOR PELLING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-13-05
PRIOR FILING DATE: 2000-01-05
NUMBER: PCT/US00/00219
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CRGANISM: HOMO
US-09-907-613-376
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703 AATTATTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTGAAC 747

Search completed: June 9, 2005, 17:44:27 Job time: 594 secs

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ALIGNMENTS

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Sequence 12936, Sequence 14724, Sequence 14578, Sequence 41762, Sequence 15691, Sequence 12008, Sequence 15666, Sequence 17056, Sequence 17504, Sequence 17504, Sequence 14590, Sequence 14590

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APPLICANT: Godowski, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Milan, Kenneth, J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret A.
APPLICANT: Roy, Margaret A.
APPLICANT: Though A.
APPLICANT: Though A.
APPLICANT: Though A.
APPLICANT: Wood, Milliam, D. Mickey
APPLICANT: WOOD A.
APPLICANT: WOOD WILLIAM DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
US-09-949-016-12936
US-09-949-016-14724
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US-09-949-016-41761
US-09-949-016-15450
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Compugen Ltd
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US-09-905-125A-376

US-09-906-775A-376

US-09-906-705A-376

US-09-901-603A-376

US-09-901-603A-376

US-09-901-618-376

US-09-901-618-376

US-09-901-618-376

US-09-901-618-376

US-09-901-618-39

US-09-389-681-29

US-09-389-681-29

US-09-618-29

US-09-389-681-29

US-09-413-826B-29

US-09-413-826B-29

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US-09-413-826B-29

US-09-413-826B-29

US-09-618-29

US-09-618-29

US-09-918-018-135

US-09-918-016-1599

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US-09-949-016-1599
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Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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Result

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726 GGTAGGAATAAATCCTTTGAACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACTCAA 785
                                                                                                                                              786 ATGTGTAAAGAAGGAAGAGCAAGAACATGGCCACACACCCCACCCCACACGAGAAATTTG 845
                                                                                                                                                                                    859 CTATCAGGCATCAGAAGGACTGCACATGTATGTATTACTGGGACATAAGTAAAAAGA 915
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US-09-905-125A-376
; Sequence 376, Application US/09905125A
· Patent No. 6664376
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Filvaroff, Ellen
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCTCTCAAA---TTTCCGGGCAGAACTTACAGCCACATAGAAATATTAAGGAGCTTTC 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 CATCTTTCAAACCTGTGATGAGAAAAGTTTCAGCTACCTGAGAATTTCACAGAGCTCTC
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Pred. No. 6.9e-105;
0; Mismatches 216;
        FRIOR TILLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
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PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-13-20
PRIOR FILING DATE: 1999-13-30
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PRIOR FILING DATE: 1999-13-30
PRIOR FILING DATE: 1999-13-30
ING DATE: 1999-09-15
LICATION NUMBER: PCT/US99/23089
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Best Local Similarity 72.9
Matches 610; Conservative
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CORGANISM: Homo Sapien
US-09-907-794A-376
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859 CTATCAGGCATCAGAAGGACTGCACATGTATGTATTACTGGGACATAAGTAAAAGA 915
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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CURRENT PILING DATE: 2001-07-10
PRIOR PELICATION NUMBER: US/09/902,775A
CURRENT PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-36
PRIOR PILING DATE: 1999-07-36
PRIOR PILING DATE: 1999-07-36
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
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PRIOR APPLICATION NUMBER: PCT/US99/2169
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/2164
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/2181
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PELING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PELING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28059
PRIOR APPLICATION NUMBER: PCT/US99/28059
PRIOR PILING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PELING DATE: 1999-12-07
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APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US00/00219
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Patent No. 6686451
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Grimaldi, Christopher J.
Gurney, Austin L.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTGTAAAGAAGGAAGAGCAAGAACATGGCCACACCCCACCGCCCACACGAGAAATTTG 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTACAGTGAGGCATCAGGTTCAGTCAAGAATTGCTGTCCTTTGAACTGGAAACATTA 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 TGGGATCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 CTGCTCAGCCATGGGGGCTCACCTGGTGTTATCAACTCACAGGAGGAGGAGGAATTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTCGCACAAAATCTAAAAGGAAAGACTTTTATATTTGGACTGACAGACCAGGTGGTGG
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PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US90/00219
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-905-125A-376
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT APPLICATION NUMBER: PCT/USO0/04414
PRIOR PRIOR PELING DATE: 2000-02-22
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
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PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 2099-12-07
PRIOR PLING DATE: 2099-13-07
PRIOR PLING DATE: 200-07
PRIOR PORTOR DATE: 200-07
PRIOR 
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                       Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan, James
Paoni, Nicholas F.
                                                                                                                                                                                                                             Gerber, Hanspeter
Gerritsen, Mary E.
                     Genentech, Inc.
Ashkenazi, Avi
Botstein, David
                                                                                          Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                     Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                             Goddard, A.
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; ORGANISM: Homo Sapien
US-09-906-700-376
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                                                                                                                                                                                                                               Indels
                                                                                                                                                                                Query Match 17.5%; Score 439.4; DB 4; Best Local Similarity 72.9%; Pred. No. 6.9e-105; Matches 610; Conservative 0; Mismatches 216;
PRIOR FILING DATE: 2000-01-05
                   NUMBER OF SEQ ID NOS: 423
SEQ ID NO 376
LENGTH: 997
                                                                                        TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                     US-09-902-775A-376
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17.5%; Score 439.4; DB 4; Length 997;

Query Match

US-09-906-700-376 ; Sequence 376, Application US/09906700 ; Patent No. 6723535

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APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Michaels F.
APPLICANT: Paoni, Michaels F.
APPLICANT: Pumas, Daniel
APPLICANT: Williams P. Mickey
APPLICANT: Williams, I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acide Encoding the Same
FILE REFERENCE: GNR.1618P2C12
CURRENT FILLING DATES 2001-07-11
CURRENT FILLING DATES 2001-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
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PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-12-02
PRIOR PPLIOR NUMBER: PCT/US99/3099
PRIOR FILING DATE: 1999-12-02
PRIOR PPLICATION NUMBER: PCT/US99/3099
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PRIOR PILING DATE: 1999-12-02
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PRIOR PRIOR PILING DATE: 1999-12-03
                                                                                                             Godowski, Paul J.
Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
                            Gerber, Hanspeter
Gerritsen, Mary E.
        Gao, Wei-Qiang
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                                    Gaps
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  72.9%; Pred. No. 6.9e-105;
iive 0; Mismatches 216; Indels
Best Local Similarity 72.9
Matches 610; Conservative
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                                                                             Gape
                                                                         11;
                                    Length 997;
                                                                         Indels
                                    Score 439.4; DB 4;
Pred. No. 6.9e-105;
0; Mismatches 216;
                                    Query Match
Best Local Similarity 72.9%;
Matches 610; Conservative C
US-09-903-603A-376
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Sequence 376, Application US/09903603A
Fatent No. 6767995
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.;
APPLICANT: Ashkenazi, Avi
APPLICANT: Desnoyers, Luc
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.

US-09-903-603A-376

RESULT 5

Ferrara, Napoleone Filvaroff, Ellen Fong, Sherman

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

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69 AGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAAATGAATTCATCTTGA
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Pred. No. 6.9e-105;
0; Mismatches 216;
                                                   APPLICANT: Fean; Nicholas F.
APPLICANT: Seawart, Timochy A.
APPLICANT: Stewart, Timochy A.
APPLICANT: Stewart, Timochy A.
APPLICANT: Stewart, Timochy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane P
TITLE OF INVENTION: Secreted and Transmembrane P
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT FILING DATE: 10466-14
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-36
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-15
PRIOR PELING DATE: 1999-10-15
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
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PRIOR PELING DATE: 1999-12-20
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Best Local Similarity 72.9%;
Matches 610; Conservative
                                     Pan, James
Paoni, Nicholas F.
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ORGANISM: Homo Sapien
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                                                             207 CGGGGCCTCCATCCTGTTTCTCAGTGGCTGTTCATCACCAGATGTCGTAACATATCG
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Patent No. 6806352
GENERAL INFORMATION:
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Ferrara, Napoleone
Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Benoyers, Luc
APPLICANT: Eaton, Dan L.
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186 TGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGAACATTTCG

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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.

APPLICANT: APPLICANT: APPLICANT:

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Acids Encoding the Same
          THILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/909,064

CURRENT APPLICATION NUMBER: US/09/909,064

CURRENT FILING DATE: 2001-07-18

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PRIOR FILING DATE: 1999-07-36

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-03

PRIOR PRILING DATE: 1999-12-
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Best Local Similarity 72.9
Matches 610; Conservative
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botslein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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                                                                                                                    11;
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Score 439.4; DB 4;
Pred. No. 6.9e-105;
0; Mismatches 216;
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; TYPE: DNA
; ORGANISM: Homo
US-09-905-381A-376
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APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,381A
CURRENT FILING DATE: 2001-07-13
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
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   426 ciecicadecaresesecreacereserserrareaacreacasesasesaseaarreer
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Patent No. 6818746
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Godowski, Paul J.
Grimaldi, Christopher J.
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Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Hillan, Kenneth,
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Beton, Dan L.
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Pred. No. 6.9e-105;
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: DCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PRILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
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PRIOR PLING DATE: 1999-12-06
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Best Local Similarity 72.9%;
Matches 610; Conservative (
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TYPE: DNA
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APPLICANT: Stewart, Timethy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Walliam, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION Acids Encoding the Same
TITLE OF INVENTION NUMBER: US/09/906,618
CURRENT APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-09-08
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                                                                       CTCCAGGAAGAACTGGAATGATACACTGTTTCTACAGTATGCCTTGGATTTGTGAGAT
TGGGGAGCCCAACAATATAGTTTTGGTGGAGGACTGTGCCCACCATAAGGGACTCTTCAAA
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
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Paoni, Nicholas F.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Benoyers, Luc
APPLICANT: Eaton, Dan L.
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Pred. No. 6.9e-105;
0; Mismatches 216;
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-00-16
PRIOR FILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-02
PRIOR PLING DATE: 1999-11-02
PRIOR PLING DATE: 1999-11-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
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Best Local Similarity 72.9%;
Matches 610; Conservative 0
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; Sequence 29, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 21012.1.470C8
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
LENGTH: 301
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Pred. No. 2.2e-31;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                            Score 157.8; DB 4
Pred. No. 2.2e-31;
0; Mismatches 55
FILE REFERENCE: 210121.470C3
CURRENT APPLICATION NUMBER: US/09/389,681A
CURRENT FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 301
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US-09-389-681-29
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nes 189; Conserv
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US-09-620-405B-29/c
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                                                                                                                                                                                                                   TYPE: DNA
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Best Local 3
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Patent No. 6387697

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Vugiu, Jiang
APPLICANT: Witcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: AND APPLICANTION NUMBER: US/09/222.575
CURRENT FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 174
SEQ ID NOS: 174
SEQ ID NO 29
LENGTH: 301
TYPE: DNA
APPLICANT: Mitcham
APPLICANT: 
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   666 CCCAAGGCAAAATTGGAATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAAT 725
                                                          744 GCCAGAAATAAGTCCTCAGGACTAAGTGCAA-----GGAAATACAAGGGACATGGCTTAC 798
                                                                                                                    726 GGTAGGAATAAATCCTTTGAACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACTCAA 785
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Sequence 29, Application US/09389681A

Patent No. 651827.

GENERAL INFORMATION:

APPLICANT: Yuqui, Jiang

APPLICANT: Micham, Jennifer L.

APPLICANT: Micham, Jennifer L.

APPLICANT: Micham, Jennifer L.

APPLICANT: Wi, Jiangchun

TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                859 CTATCAGGCATCAGAAGACTGCACATGTATGTATTACTGGGACATAAGTAAAAAGA 915
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Pred. No. 2.2e-31;
0; Mismatches 52;
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Best Local Similarity 78.4%;
Matches 189; Conservative (
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US-09-222-575-29/c
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CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 474
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
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US-09-604-287A-29
                                                                       LENGTH: 301
TYPE: DNA
ORGANISM: Homo sapien
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301 TITIATIGGACTGICAGACCAGGITGICGAGGITCAGIGGCAAIGGGIGGACGGCACACC 242
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                                                        714 TTTCTACAGTATGCCTTGGATTTGTGAGATGCCAGAAATAAGTCCTCAGGACTAAGTGCA 773
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Patent No. 6579973
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqui
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangcham, Jennifer L.
APPLICANT: Xu, Jiangcham, Jennifer L.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121-4700c4
CURRENT APPLICATION NUMBER: US/09/433,826B
                                                                                                                                                                                                                                                                                               APPLICANT: Vidiu, Jiang
APPLICANT: Micham, Jennifer L.
APPLICANT: Micham Composition of Their Use THILING PARTHOLS FOR THEIR USE CURRENT APPLICATION NUMBER: US/09/339,338A
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                            534 TTATATTGGACTGACAGACCAGGTGGTGGAGGGTCAGTGGCAATGGGAGGATGATACACC
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Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels
                                                                                                                                                                                                                                            ; Sequence 29, Application US/09339338A; Patent No. 6573368; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-433-826B-29/c
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US-09-339-338-29
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Length 301;
Query Match 6.3%; Score 157.8; DB 4; Length Best Local Similarity 78.4%; Pred. No. 2.2e-31; Matches 189; Conservative 0; Mismatches 52; Indels
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; Sequence 29, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; TITLE OF INVENTION: DIAGNOSIS OF BREAST
; CURRENT PAPLICANTON NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
; LEASTTH: 301
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 714 TITCTACAGTATGCCTTGGATTTGTGAGATGCCAGAATAAGTCCTCAGGACTAAGTGCA
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 Db
 121 TITCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTGAACAAAGGAAA
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Search completed: June 9, 2005, 09:46:00 Job time: 433 secs

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| Beguence 1, Application US/10812620
| Publication No. US20050019860A1
| GENERAL INFORMATION:
| APPLICANT: Japan Science and Technology Corporation
| TITLE OF INVENTION: A novel C-type lectin and its genes
| FILE REFERENCE: JA904071
| CURRENT APPLICATION NUMBER: US/10/110,945
| PRIOR FILING DATE: 2004-03-29
| PRIOR FILING DATE: 2002-04-14
| PRIOR FILING DATE: 1999-10-15
| NUMBER OF SEQ ID NOS: 2
| SEQ ID NO 2: 2
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US-09-906-742-376
US-09-907-613-376
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US-09-907-913-376
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Best Local Similarity
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and is derived by analysis of the total score distribution.
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Sequence 21733
Sequence 40, Ap
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                              CTGCTACAATTATGGATCAGGTTCAGTCAAGAATTGTTGTTGTTGAACTTGGGAATATTT
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                                                                                                                                                                                                                                                TGTACATTAGGTTACAGAAAAAACAACTTTAGCCACAAAAATAAAGTAATAAACTATT 2517
                                                                                                                                                                                                                                                                  Sequence 21733, Application US/09814353
| Publication No. US20030165831A1
| GENERAL INFORMATION:
| APPLICANT: Let, John
| APPLICANT: Lillib. Jamela
| APPLICANT: Lillib. Jamela
| APPLICANT: Lillib. Jamela
| APPLICANT: Lillib. Jamela
| APPLICANT: Lillib. Jamela
| APPLICANT: Lillib. Jamela
| APPLICANT: Lillib. Jamela
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
| TILLE OF INVENTION: THERAPY OF OVARIAN CANCER
| TILLE OF INVENTION: THERAPY OF OVARIAN CANCER
| TILLE OF INVENTION: THERAPY OF OVARIAN CANCER
| TILLE OF INVENTION: TOOGO 13-21
| CURRENT APPLICATION NUMBER: US 60/191,031
| PRIOR FILLING DATE: 2000-03-21
| PRIOR FILLING DATE: 2000-06-15
| PRIOR PLICATION NUMBER: US 60/216,820
| PRIOR PLICATION NUMBER: US 60/216,820
| PRIOR FILLING DATE: 2000-07-07
| PRIOR FILLING DATE: 2000-07-07
| PRIOR FILLING DATE: 2000-07-25
| PRIOR PELICATION NUMBER: US 60/257,672
| PRIOR PELICATION NUMBER: US 60/257,672
| PRIOR PELICATION NUMBER: US 60/257,672
| PRIOR PELICATION NUMBER: US 60/257,672
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                                     AAACTGAAGGGATCATGATAGATAACTTTTGGATCTTTTCACTTTTCTATTGCTGGATG
                                                                                          AAACATGACCCGAAACTATCTTGGGCCGGGAAAATTTTAATTTATCTTAACATAAATTTC
                                                                                                                                                                     CTATTTAGAAATTGGACAGGTGGGGAATCATCCAATTGAAACTCGAAAATGTAGTGTTT
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LOCATION: 1, 2143
OTHER INFORMATION: n = A,T,C or G
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                                                 482 CTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGGAGGAATTCCT
                                                                                                            TTTTCGCACAAAATCTAAAAGGAAAGAGTTTTATATTTGGACTGACAGACCAGGTGGTGGA
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OTHER INFORMATION: Incyte ID No. US20030124649A1 1521513CB1
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GENERAL INFORMATION:
APPLICANT: LAL, Preect; YUE, Henry
APPLICANT: TANG, Y. Tom; BANDMAN, Olga
APPLICANT: BUREORD, Neil; AZIMZAI, Yalda
APPLICANT: BUGGN, Neil; AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.;
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PP-0731-1 USA
CURRENT APPLICATION NUMBER: US/09/969,680A
CURRENT FILING DATE: 2001-10-02
PRIOR PLING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 40
LENGTH: 968
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73.0%; Pred. No. 9.7e-96;
tive 0; Mismatches 215;
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; Sequence 40, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
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Matches 611; Conservative
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ORGANISM: Homo sapiens
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                                             1351 -TICCIGGAGCCCCATITICICIGIGIICTCTTCTATAAAC----IGGAITICACCIGIA 1405
                                                                                   1431 ATCCCTGGGGCTTCCTTTGCTCTGCCTTATTTTCAATTGACTGAATGGATCTCACCAGAT 1490
                                                                                                                                1406 CTTGTATCTACTGCGCAAGTAGAACCTGCTCAGTAGGTTCAAAGTGAAATTATTTAAAAA 1465
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1371 CCTTCTTAGGGAAGGGCATGCCAGCCATCAGCTCCAAACAGGCTGTAACCAAGTCCACCC 1430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 TGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTCG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 CAGCICTCAAA---TITCCGGGCAGAACTIACAGCCACATAGAAATATTAAGGAGCTTTC 323
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APPLICANT: Lal. Preeti
APPLICANT: Tal. Henry
APPLICANT: TANG, Y. Tom
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: D'YUNG AIMA M.
APPLICANT: PATTERSON, Chandra
ITILE OF INVENTION MENBRANE ASSOCIATED PROTEINS
FILE OF INVENTION NUMBER: US/09/965,529
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/149,641, 60/164,203; PCT/US00/22315
PRIOR PPLING DATE: 1999-017; 1999-11-09; 2000-08-14
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL PROGRAM
SEQ ID NO 40
LENGTH: 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 17.5%; Score 441; DB 9; Length 968; Il Similarity 73.0%; Pred. No. 9.7e-96; 611; Conservative 0; Mismatches 215; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 1521513CB1
US-09-965-529-40
                                                                                                                                                                                                                                            1550 TICATCTCCACACTTTCCTGTCTCAAGCC 1578
                                                                                                                                                                                                                      1466 TICATGITCACATTITICIGICICAGGAC 1494
                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/09965529
Publication No. US20020182671A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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Best Local S
Matches 611
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APPLICANT: Kijaturi, Nemieer, J.
APPLICANT: Kijaturi, Nemieer, J.
APPLICANT: Kijaturi, Varia S.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, Jamae P.
APPLICANT: Pan, Jamae P.
APPLICANT: Pan, Jamae P.
APPLICANT: Pan, Jamae P.
APPLICANT: Roy, Magratet Ann
APPLICANT: Tumae, Daniel
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APPLICANT: 
        Hillan, Kenneth, J
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CTCCAGGAAGAACTGGATAATCCCTGTTTCTACAGTATGCCTTGGATTTGTGAGAT
                                                                                      CGGGGCCTCCATCCTGTTTCTCAGTGGCTGTTTCATCACCAGATGTGTCGTAACATATCG
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                                                                                        147 ATCCCACCACACAGAGAGAGATGCTTCAAAAACTCCCAAGTGCTCTCCTGGACGATAGC
                                                                                                                                   Gaps
                        11;
  Length 997;
                       Indels
Score 439.4; DB 9;
Pred. No. 2.4e-95;
0; Mismatches 216;
Query Match
17.5%;
Best Local Similarity 72.9%;
Matches 610; Conservative 0
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; ORGANISM: Homo Sapien US-09-909-320-376

Sequence 376, Application US/09909320 Patent No. US20020132240A1 GENERAL INFORMATION:

RESULT 5 US-09-909-320-376

Goddard, A. Godowski, Paul J. Grimaldi, Christopher J. Gurney, Austin L.

Gerber, Hanspeter Gerritsen, Mary E.

Ferrara, Napoleone Filvaroff, Ellen Fong, Sherman

APPLICANT: Genentech, Inc.
APPLICANT: Abkenazi, Avi
APPLICANT: Betstein, David
APPLICANT: Bestow, Dan Lu
APPLICANT: Beton, Dan Lu
APPLICANT: Ferrara, Napoleone
APPLICANT: Forg, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gooder, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Godwaki, Paul J.
APPLICANT: Godwaki, Paul J.
APPLICANT: Grimaldi, Christop
APPLICANT: Grimaldi, Christop

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AGAGAGAGAGAAAAAAAGAGAGAGAGAAAAAAAAAATGAATTCATCTAAATCATCTGA 128
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Pred. No. 2.4e-95;
0; Mismatches 216;
                  TITLE OF INVENTION: Secreted and Transmembrane P TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/09,088B CURRENT FILING DATE: 1046-122 VO00-02-22 VO00-0414 PRIOR PELICATION NUMBER: PCT/US00/04414 PRIOR FILING DATE: 1999-07-07 PRIOR APPLICATION NUMBER: US 60/145,698 PRIOR FILING DATE: 1999-07-26 PRIOR APPLICATION NUMBER: US 60/146,222 PRIOR APPLICATION NUMBER: PCT/US99/20594 PRIOR FILING DATE: 1999-09-13 PRIOR PILING DATE: 1999-09-13 PRIOR FILING DATE: 1999-09-13 PRIOR PILING DATE: 1999-09-13 PRIOR PILING DATE: 1999-09-13 PRIOR PILING DATE: 1999-09-13 PRIOR APPLICATION NUMBER: PCT/US99/28313 PRIOR PILING DATE: 1999-10-05 PRIOR APPLICATION NUMBER: PCT/US99/28313 PRIOR FILING DATE: 1999-11-29 PRIOR PILING DATE: 1999-11-29 PRIOR PILING DATE: 1999-11-29 PRIOR PILING DATE: 1999-11-29 PRIOR PILING DATE: 1999-11-20 PRIOR FILING DATE: 1999-11-20 PRIOR FILING DATE: 1999-11-20 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-07 PRIOR FILING DATE: 1999-12-07 PRIOR FILING DATE: 1999-12-07 PRIOR FILING DATE: 1999-12-07 PRIOR FILING DATE: 1999-12-07 PRIOR FILING DATE: 1999-12-07 PRIOR FILING DATE: 1999-12-07 PRIOR FILING DATE: 1999-12-07 PRIOR FILING DATE: 1999-12-07 PRIOR FILING DATE: 1999-12-07 PRIOR FILING DATE: 2000-01-05 PRIOR FILING DATE: 2000-01-05 PRIOR FILING DATE: 2000-01-05 PRIOR FILING DATE: 2000-01-05 PRIOR FILING DATE: 2000-01-05 PRIOR FILING DATE: 2000-01-05 PRIOR FILING DATE: 2000-01-05 PRIOR FILING DA
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CORGANISM: Homo Sapien
US-09-909-088B-376
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Best Local Similarity
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306 ciectacaarrarggarcaggircagrcaagaarrgrigrccarrgaacreggaararr 365
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Patent No. US20020146709A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goddard, A.
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US-09-909-088B-376
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TCAATCCAGCTGCTACTTCTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAA 425
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                                                                                                                        426 CTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCT
                                                                                                   TTTTCGCACAAAATCTAAAAGGAAAGAGTTTTATATTGGACTGACAGACCAGGTGGTGGA
                                                                                                                                                                        GGGTCAGTGGCAATGGGAGGATGATACACCTTTCACAGAGTCCCTGACCTTCTGGGATGC
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CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PLING DATE: US 60/143,048
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Stewart, Timothy A.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Mather, Jennie P
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Pred. No. 2.4e-95;
0; Mismatches 216;
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
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ORGANISM: Homo Sapien
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US-09-902-853-376
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Best Local Similarity
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                                                                                                                                                       CCCAAGGCAAAATTGGAATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAAT 725
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                                                                                   606 AGGGAGCCCAACAACATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAA
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GGGTCAGTGGCAATGGGAGGATGATACACCTTTCACAGAGTCCCTGACCTTCTGGGGATGC
                    546 GGGTCAGTGGGAATGGGACGGCACACCTTTGACAAGTCTCTGAGCTTCTGGGATGT
                                                             624 TGGGGAGCCCAACAATATAGTTTTTGGTGGAGGACTGTGCCACCATAAGGGACTCTTCAAA
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APPLICANT: Part Dames
APPLICANT: Part, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Secreted and Transmembrane
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TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Secreted and Transmembrane
FILING DATE: 1000-09-18
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 376, Application US/09902853
Publication No. US20020192659A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Gerritsen, Mary E.
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APPLICANT: Ashkenari, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wei-Qiang
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Pred. No. 2.4e-95;
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-11-00
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PRIOR FILING DATE: 200-01-05
NUMBER OF SEQ ID NOS: 423
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Pred. No. 2.4e-95;
0; Mismatches 216;
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
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ORGANISM: Homo Sapien
US-09-907-824-376
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Matches 610; Conserv
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APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wool, William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: Wool, William, P. Mickey
APPLICANT: Wool, William, P. Mickey
APPLICANT: Wool, William, P. Mickey
APPLICANT: Wool, William, P. Mickey
APPLICANT: Wool, William, P. Mickey
APPLICANT: Wool, William, P. Mickey
APPLICANTON: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Secreted and Transmembrane
APPLICANT: Wool, William, I.
ITLE OF INVENTION: Secreted and Transmembrane
FRICK APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2000-09-18
PRIOR FILING DATE: 1099-00-02
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-00-08
PRIOR FILING DATE: 1999-00-08
PRIOR PAPLICATION NUMBER: PCT/US99/21090
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/2184
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/2184
PRIOR PLING DATE: 1999-09-15
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                                             666 CCCAAGGCAAAATTGGAATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAAT 725
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        CTCCAGGAAGAACTGGAATGATAATCCCTGTTTCTACAGTATGCCTTGGATTTGTGAGAT
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Publication No. US20020197671A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-15
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                                   ATGCATGAAGAAGAACAAGAGTGAATGTAATAACAACCAAAAATCCAACATAAGAAAATAT 858
                                                                                                                    846 TGCGCTGAACTTCAAAGGACTTCATAAGTATTTGTTACTCTGATACAAATAAAATA 902
                                                                             859 CTATCAGGCATCAGAAGGACTGCACATGTATGTATTACTGGGACATAAGTAAAAAGA
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 376
LENGTH: 997
TYPE: DNA
ORGANISM: Homo Sapien
US-09-907-841-376
                                                                                                                                                                                                                  Sequence 376, Application US/09907841
PUBlication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bostetain, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, David
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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US-09-907-841-376
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                                                                                              ATCCCACCACACAGAGAGAGGATGCTTCAAAAACTCCCAAGTGCTCTCCTGGACGATAGC
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                                                 Gaps
                                               Indels 11;
  Length 997;
Score 439.4; DB 9;
Pred. No. 2.4e-95;
0; Mismatches 216;
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Publication No. US2030003530A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Abthemazi, Avi
APPLICANT: Botsein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
APPLICANT: Faston, Dan L.
APPLICANT: Faston, Dan L.
APPLICANT: Filvaroff, Ellen
17.5%;
72.9%;
Query Match 17.5
Best Local Similarity 72.9
Matches 610; Conservative
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US-09-904-011-376
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129 AACACAATGCACAGAGGATGCTTC---TCTTCCCAAATGTTCTTATGGACTGTTGC 185
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  ATCCCACCACCACAGAGAGAGGATGCTTCAAAAACTCCCAAGTGCTCCTGGACGATAGC
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICANT: ROY, MAYBEEC ALL
APPLICANT: Walliam, T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
PRIOR APPLICATION NUMBER: US 00/414
PRIOR PRIOR PAILS 0000-09-18
PRIOR PRIOR PRINCH DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PRIOR DATE: 1999-07-26
PRIOR APPLICATION NUMBER: DCT/US99/2094
PRIOR PRIOR DATE: 1999-07-36
PRIOR PRIOR DATE: 1999-09-15
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72.9%; Pred. No. 2.4e-95;
tive 0; Mismatches 216; Indels
                                                                                             Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
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Best Local Similarity 72.9
Matches 610; Conservative
                                                                        Goddard, A.
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CORGANISM: Homo Sapien
US-09-904-011-376
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744 GCCAGAAATAAGTCCTCAGGACTAAGTGCAA----GGAAATACAAGGGACATGGCTTAC 798
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                                                                                                   ATGCATGAAGAAGAACAAGAGTGAATGTAATAACAACCAAAAATGTAAGAAAATAT 858
                                                                                                                                859 CIATCAGGCATCAGAAGGACTGCACATGTATGTATTACTGGGACATAAGTAAAAAGA 915
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CURRENT APPLICATION NUMBER: 09/665,350
PRIOR PLILING DATE: 2001-07-17
PRIOR PLLING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-07-07
PRIOR PLILOGATION NUMBER: 05 60/145,698
PRIOR PLILOGATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-18
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PRIOR PLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28314
PRIOR PLING DATE: 1999-11-30
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PRIOR PLING DATE: 1999-11-30
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Grimaldi, Christopher
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gerritsen, Mary E.
Goddard, A.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION NUMBER: US/09/903,640
CURRENT APPLICATION NUMBER: US/09/903,640
PRIOR FILING DATE: 2001-07-11
PRIOR PLLING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.5%; Score 439.4; DB 10; Length Best Local Similarity 72.9%; Pred. No. 2.4e-95; Matches 610; Conservative 0; Mismatches 216; Indels
                        Hillan, Kenneth, J
                                             Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-640-376
                                                                                                   Pan, James
                                                                     APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Mather, Jennie P.
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APPLICANT: Ban, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Sceneral and Transmembrane Polypeptides and Nucleic
CURRENT FILING DATE: 10466-11 (1909) 906.742
CURRENT FILING DATE: 1004-07-16
FILIS REFERENCE: 10466-11 (1909) 906.742
CURRENT FILING DATE: 2000-00-318
FRIOR PAPLICATION NUMBER: 09665,350
FRIOR PAPLICATION NUMBER: 09665,350
FRIOR PAPLICATION NUMBER: 0960/144,488
FRIOR APPLICATION NUMBER: 0960/146,222
FRIOR PAPLICATION NUMBER: 1999-07-28
FRIOR PAPLICATION NUMBER: 1999-07-28
FRIOR PAPLICATION NUMBER: 1999-07-28
FRIOR PAPLICATION NUMBER: PCT/US99/2094
FRIOR PAPLICATION NUMBER: PCT/US99/2199
FRIOR PAPLICATION NUMBER: PCT/US99/2199
FRIOR PAPLICATION NUMBER: PCT/US99/2199
FRIOR PAPLICATION NUMBER: PCT/US99/2199
FRIOR PAPLICATION NUMBER: PCT/US99/2199
FRIOR PAPLICATION NUMBER: PCT/US99/2199
FRIOR PAPLICATION NUMBER: PCT/US99/2199
FRIOR FILING DATE: 1999-09-15
FRIOR PAPLICATION NUMBER: PCT/US99/2199
FRIOR FILING DATE: 1999-11-29
FRIOR APPLICATION NUMBER: PCT/US99/31095
FRIOR APPLICATION NUMBER: PCT/US99/31091
FRIOR APPLICATION NUMBER: PCT/US99/31091
FRIOR APPLICATION NUMBER: PCT/US99/31091
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FRIOR APPLICATION NUMBER: PCT/US99/31091
FRIOR APPLICATION NUMBER: PCT/US99/31091
FRIOR APPLICATION NUMBER: PCT/US99/31091
                               Sequence 376, Application US/09906742; Publication No. US20030023054A1; GENERAL INFORMATION:
APPLICANT: Genencech, Inc.; APPLICANT: Ashkenazi, Avi; APPLICANT: Bostein, David; APPLICANT: Bestein, David; APPLICANT: Bestoop
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Gao, Wei-Diang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                 Ferrara, Napoleone
Filvaroff, Ellen
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Mather, Jennie P.
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Pred. No. 2.4e-95;
0; Mismatches 216; Indels 11;
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-16
PRIOR PRILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
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NUMBER OF SEQ ID NOS: 423
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72.9%;
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Best Local Similarity 72.9
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                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo Sapien
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US-09-908-093-376
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                                                                                                                                                                                                                        17.5%; Score 439.4; DB 10; Length 997; 72.9%; Pred. No. 2.4e-95; tive 0; Mismatches 216; Indels 11;
PRIOR APPLICATION NUMBER: PCT/US99/30999;
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219;
PRIOR PILING DATE: 2000-01-05;
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 376
LENGTH: 997
TYPE: DNA
TYPE: DNA
ORGANISM: HOMO Sapien
US-09-906-742-376
                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.9
Matches 610; Conservative
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/906,838

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-02-22

PRIOR PELING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

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PRIOR FILING DATE: 1999-12-20

PRIOR PRIOR PRIOR DATE: 1999-12-30
Sequence 376, Application US/09906838 Publication No. US20030027143A1 GENERAL INFORMATION:
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Godowski, Paul J.
Grimaldi, Christopher
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                         APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dan L.
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186 TGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTCG 245
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Best Local Similarity 72.9%; Pred. No. 2.4e-95;
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-838-376
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61 TTCCAGGGGCTCTTTCTAAACTGAGAAGAAGGAAAAGGAAGAAAAGGCAGGAAAAAAGGA 120
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ilve 0; Mismatches
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Novel C lectin and gene thereof.
E54035
E54035. I GI:22553489
JP 2001112482-A/1.
Mus sp.
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    /db_xref="taxon:10095"

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Best Local Similarity 100.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Oy 2461 IGTACATTAGGTTACAGAAAAACAACTTTAGCCACAAAAATAAAGTAATAAACTATT 2517 	RESULT 3 AB024717 LOCUS AB024717 LOCUS DEFINITION WE musculus mRNA for macrophage C-type lectin Mincle, complete ACCESSION AB024717 VERSION AB024717 VERSION AB024717	_		A moved in macrophages J. Immunol. 163 (9), 5039-5048 (1999) 99458965	REFERENCE 1 (bases 1 to 2517) Pwb. 11/1/99 AUTHORS Akira,S. and Matsumoto,M. TITLE Direct Submission	JOUKNAL SUBMILTEGG (1974RAF.199) SAIZIOO AKKIRA, USAKA UNIVEESLY, DEPAILMENT OF HOST DEFENSE, RESEATCH INSTITUTE for Microbial Diseases; 3-1 Yamada-oka, Suita, Osaka 55-0871, Japan (E-mail:sakira@biken.osaka-u.ac.jp, Tel:81-6-6879-8303,	FEATURES rax:81-6-84/95) FEATURES 1. Cation/Qualifiers 1. C.2517 /organism="musculus"	/mo.ref="mkNA" /db_xref="taxon:10090" 12517 /gene="Mincle"		/ procein la="BAAB3/94.1" / db xref="d1:5821286" / translation="MNSTKSPASHHTERGCFKNSQVLSWTIAGASILFLSGCFITRCV		Query Match 98.9%; Score 2489.8; DB 10; Length 2517; Best Local Similarity 99.3%; Pred. No. 0; Matches 2500; Conservative 0; Mismatches 17; Indels 0; Gaps	1 CGGTCTGTACTCTTGAACTTTTAAAAGAGGGCCAGGATTCACCATTCAAGACTCACT 		Qy 121 AGAATGAATTCAACCAAATGGCTGCATCCCACCACACAGAGAGGATGCTTCAAAAC 180	Qy 181 TCCCAAGTGCTCTGGACGATAGCCGGGGCCTCCATCCTGTTTCTCAGTGGCTGTTTC 240
OY 1381 TTCTATAAACTGGATTTCACCTGTACTTGTATCTACTGGGCAAGTAGAACCTGGTCAGTA 1440 	1441 GGTTCAAAGTGAAATTATTAAAAATTCATGTTCACATTTTTCTGTCTCAGGACTGCATT 1500	1561 TTCAGCAGCAGTCACACATTGTAATAAACATGTATCCTTGAGTAGGAAAATTAAACTAAA 1620 	1621 TAAATTAATTTGTCATATTAGCACTCATTACGAGCACTTCTATTAGACTTTCTCACAATC 1680 	1681 TGATTITGAAATTGATAACCTTATTITAAATACAAATATATCTTACAACCACACATTTGA 1740 	1741 CTTCTTTTTAAARTATTTTGTTTGAAARTTTTGTGCATTTATATATACACTTTTA 1800 	1801 ATGAACCCATCCTTACTCTCCACTACAACCTGCTCCTATCCACCTCACTGATTTTCCC 1860	1861 TCCCAATTTCATGTGCTCCTCTTTGTTTTAAACCCACTCTATCTGCTCAGTGCTTCCTGA 1920 	1921 ATGCACTTGAGTATAAGGCTTTCTACTGGACCATAGCCTCTCGGCAACCACATCCCATAC 1980 	1981 TCCACCTGCTCCAGCAGGAACAATAGCCAATTGACCATCTTCAGCTGAGGATGGAT	2041 ATGAGCTCCATGCCATTCATGCTGGAATTTGGGTTGTTTTATGTAACCTTTATTATATTG 2100 	2101 IGCTATCTCTTCTGTATCCCTAGAATCTCTAGGAGCTTCATATTAAAAGATTCTGAATTC 2160 	2161 CATCAAAGGGCACACAAAGAAATCACAAAGACCATGTGGTTTTTGGGTTTATTT 2220 	2221 GCAAGGTTCATTACACTCCTTGACTTGTATATATTGTGACATCCCTCCATCTCTAGGATG 2280 	2281 AAACTGAAGTGATGATAGATAACTTTTGGATCTTTTCACTTTTCTATTGCTGTGATG 2340	CATAAATTTC	CTATTTAGAAATTGGACAGGTGGGGAATCATCCAATTGAAACTCGAAAAATGTAGTGTTT

1321 GTTCCTAACAGATTGTGAACTACCACTTCCACTACCAGCCCCATTTCTCTCTGGGACCTCTGTGTT 1440 1381 TTCTATAACTGGAATTTCACCTGTAACTTGTACTCCCCAGAGCACCTCTCTGTT 1440 1381 TTCTACAACTGGAATTTCTAACATTGTACTCCACTTCTGTCTCTGTCTCACTTCTGTTTTTTTT
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SOURCE ORGANISM

VERSION KEYWORDS

ACCESSION

TITLE JOURNAL REFERENCE AUTHORS TITLE

AUTHORS

REFERENCE

JOURNAL REFERENCE TITLE JOURNAL

AUTHORS

AC124563/c LOCUS DEFINITION

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The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The Clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41. .. 191 note="Sequence derived from one plasmid subclone.
                                                                                                                                                                                                                                       NEICHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                           1. 210092
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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710<u>6</u>. .17158
                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="6"
/map="6"
/clone="RP23-206B15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="RPCI-23"
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19886. .20388
/rpt_family="ERVK"
21469. .21573
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5211. .5462
/rpt_family="ERVK"
5449. .5582
/rpt_family="ERVK"
/rpt_family="ERVK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0530. .8982
/rpt_family="ERVK"
/2521. .13567
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7286. .17534
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/rpt_family="ERVK"
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rpt_family="MaLR"
5254. .15521
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6957. .17102
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11576. .21729
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3732. .13981
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2395. .3280
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/rpt_family="L1"
2046. .2186
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141
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3456. .13694
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3250. .13448
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4058. .14453
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8783. .18936
http://genome.wustl.edu
                                             SOURCE INFORMATION:
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                                                                                                                                                                                          ROD 25-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing of Mus musculus
Unpublished (2001)
Unpublished (2001)
3 (Dases 1 to 210092)
MCPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (Dases 1 to 210092)
MCPherson, J.D. and Waterston, R.H.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-APR-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 210092)
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Submitted (29-UDL-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
(Dases 1 to 210092)
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                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 210092)
Abbott; and Meyer,R.
The sequence of Mus musculus BAC clone RP23-206B15
Unpublished (2001)
                                          2461 TGTACATTAGGTTACAGAAAACAACTTTAGCCACAAAAATAAAGTAATAAACTATT 2517
                    2461 TGTACATTAGGTTACAGAAAAACAACTTTAGCCACAAAAATAAAGTAATAAACTATT 2517
                                                                                                                                                                                       AC124563 210092 bp DNA linear ROD 25-NOV-
Mus musculus BAC clone RP23-206B15 from chromosome 6, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 On Jul 29, 2003 this sequence version replaced gi:29837778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: M BA0206B15
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                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                    AC124563.4 GI:33300796
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REFERENCE AUTHORS TITLE

JOURNAL

AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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128061 TCCAACAGTGAGGAAGATGCATCTTTGAGTCTTTAAACTTACCTGCCGCTTGGGGAGAATG 128002
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55137. .25184
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26462. .26479
2634. .26849
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73522. .23560
2461. .25030.
                                                                                                                                note="Sequence derived from one plasmid subclone."
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28616. 29012
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2935. 30359
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30441. 30587
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Contect: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Techhologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Center
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contect: amgobon.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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SLSFWDAGEPNNIVLVEDCATIRDSSNSRKWMDIPCFYSMPWICEMPEISPLD"
McKernan, K. J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S.W.,
Worllalon, D.K., Murzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketreman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, X.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 6 Row: 1 Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9910161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Straubberg, R.
Direct Submission
Direct Submission
Submitted (20-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
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Pred. No. 0;
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82._.726
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98.9%;
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TITLE
JOURNAL
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Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E (bases 1 to 1606)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haieh, F.,

Diatchenko, L., Marusina, K., Bonaldo, M.F., Casavant, T.L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
                                                                             127041 TCATTACACTCCTTGACTTGTATATTGTGACATCCCTCCATCTCTAGGATGAAACTGA 126982
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Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9, mRNA (cDNA clone MGC:5682 IMAGE:3158063), complete cds.
                                        CCATGCCATTCATGCTGGAATTTGGGTTGTTTTATGTAACCTTTATTATATTGTGCTATC
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BC003218
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non,E.,
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chen,Z., Chu,J.,
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er,T., Garza,M.,
ren,M., Guevara,W.,
hamilton,K.,
nandez,J.,
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on,R., Jolivet,A., TCTCCATATGGA 1302 ||||||||||||| TCTCCATATGGA 1260 TTCCTGGAGCCC 1362 GTTTCTTCCAG 1542 HTG 11-OCT-2002 3 IN PROGRESS Euteleostomi;

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Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

on Oct 9, 2002 this sequence version replaced gi:21744187.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold') within each contig-scaffold'). Within each contig-scaffold by sized gaps filled with Ns to the estimated and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Li, Z., Liu, J., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Lorlneged, H., Lozado, R.J., Lu, X., Ma, J., Loulneged, H., Lozado, R.J., Lu, X., Mangum, A., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mahiner, S., Marchine, E., Menen, E., Morce, S., Morgan, M., Morris, K., Martin, R., Martinez, E., Milosavijevic, A., Miner, G., Minja, E., Moneemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Norris, S., Naackervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Naackelemeh, O., Okwnon, G., Olarnpuneagoon, A., Pal, S., Pantervis, C., Neal, D., Newton, N., Mguyen, N., Norris, S., Panter, M., Perez, A., Perez, L., Pfannkoch, C., Panter, M., Pondetrer, R., Pondetrer, M., Reeves, K., Regier, M.A., Reigh, R., Pondetrer, R., Pondetrer, M., Revers, K., Regier, M.A., Reilly, M., Ren, Y., Rose, M., Rose, M., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruis, S., Shen, H., Shetty, J., Shvartebeyn, A., Steonla, R., Sodergren, E., Song, X.-Z., Sort, G., Shatsman, S., Shen, H., Steongren, E., Song, X.-Z., Sort, G., Shatsman, S., Shen, Wang, G., Wang, S., Warren, M., Warren, Y., Walker, B., Wang, J., Walge, S., Warren, W., Walter, K., Walter, R., Walter, K., Walter, R., Walter, R., Walter, K., Walter, R., Walter, R., Walter, R., Walter, R., Walter, R., Walter, R., Walter, R., Walter, R., Smith, H.O., Williasn, G., Walses, R., Smith, D., R., Smith, H.O., Williasion
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
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Submitted (08-FBB-2002) Human Genome Sequencing Center, Department
Submitted (08-FBB-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (Dases 1 to 222035)
Rat Genome Sequencing Consortium.
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2 (bases 1 to 222035)
Worley, K.C.
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AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

TITLE JOURNAL REFERENCE

18815 CATGAGGGACTCTTCAAACCCCAGGAAGAACTGGAATGATGTATCCTGTTTCTTCAGTAT 18874 18875 GCCTTGGATTTGTGAGATGCCAGAATAAGTCCTTTGGACTAGGTGCAAGGGAACACAGA 18934 18935 AGACATGGTTTACATGCACAAGGAAGAACAAAAGTGAAGGTAACAACACCTAAAATCCAA 18994 1076 18755 CCACAGCTTCTGGGATGCTGGAGAGCCCAATAACATAGTTTTTGTGGAGGACTGTGCCAC 18814 965 AACCTGAAAGATCTCTTTTAGACTGTACAGATCAATTCTCTAACAAATGCAACAAGAAG 1024 905 726 GCCTTGGATTTGTGAGATGCCAGAAATAAGTCCTCAGGACTAAGTGCAAGGAAATACAAG 906 AGTAAAAAGA-CTTGTTCCCATTGCTAAAAGTCCACAGCATTGTCTGATGGTCTTGCCAT 1025 AAAGGGATTCTCCTTTTCACATCTGTCTTGCACATCTGTCTTGCTCATGAG-----A 786 GGACATGGCTTACATGCATGAAGAAGAACAAGAGTGAATGTAATAACAACCAAAATCCAA 666 CATAAGGGACTCTTCAAACTCCAGGAAGAACTGGAATGATAATCCTGTTTCTACAGTAT Gaps NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. 43; Length 222035; 1 7987: contig of 7987 bp in length 988 8087: gap of unknown length 520 11519: contig of 3432 bp in length 620 175535: contig of 163916 bp in length 536 175535: gap of unknown length 636 222035: contig of 46400 bp in length 640 Qualifiers Indels 46.6%; Score 1173; DB 2; 80.5%; Pred. No. 6.5e-238; iive 0; Mismatches 335; CCTGACCTTCTGGGATGCTGGGGAGCCCAACAATATAGTT 1. .222035 /organism="Rattus norvegicus" /mol_type="genomic DNA" /db_xref="texon:10116" .162152) /note="wgs_contig"
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Rattus norvegicus macrophage-inducible C-type lectin (Clecsf9)
mRNA, complete cds.
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Flornes, L.M., Bryceson, Y.T., Spurkland, A., Lorentzen, J.C.,
Dissen, E. and Fossum, S.
Identification of lectin-like receptors expressed by antigen
presenting cells and neutrophils and their mapping to a novel gene
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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2144 TAAAAGATTCTGAATTCCATCAAAGGCCACACAAAGAAATCACAAAGACCATGTGGTTTC
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/receptor gene complex; APLEC"
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Flornes, L.M., Dissen, E. and Fossum, S.
Direct Submission
Direct Submission
Blindern, Oslo 0317, Norway
Location/Qualifiers
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Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
Kits, such as nucleic acid arrays, comprising a majority of
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18.3%; Score 461.4; DB 6;
Best Local Similarity 63.4%; Pred. No. 3.1e-87;
Matches 934; Conservative 0; Mismatches 466;
WO 02068579-A 3765 06-SEP-2002;
ration (NY) (US)
                                                                                                                                                                                              1. .2144
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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E. Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adame, C., Alder, J.,
Allen, C., Allen, H., Albbrookes, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Albrookes, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B. Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregoorgis, E., Geer, K., Galli, R., Garcia, A., Garner, T.,
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246843 bp DNA linear HTG 15-NOV-2002
Rattus norvegicus clone CH210-97B16, *** SEQUENCING IN PROGRESS
***, 5 unordered pieces.
                                         971 AAAGATCTCTTTTTAGACTGTACAGATCAATTCTCTAACAAATGCAACAAGAAGAAAGGG 1030
                                                                                                                                                                                                                                                                                                                                                   1091 AGAGGTAGAAAGCAGATGTCTGTATAAAGAGACTTTAAT----GGTCACTATGTCATCT 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                     1129 AGGGGATTTTGGAAGGTGCCTTCCAAAATCTCCTGAATCCGGCTCTGTAGCAGGTCCT 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1147 GTTCTTTCTACATCCTTGGCTCTAGCTTATCTATCTATCAGTACATAGATCACTTCTGTG 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1287 GACATCTCCATATGGAAAGGCCGGTCAAACTTCAGTTCCTAACAGATTGTGATCTAGTCC 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1368 TGCACCTTCTTAGGGAAAGGCATGCCATCAGCTCCAAACAACGTTCTAACAACAACAGCTCTAACAACAACAGCATCC 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1347 ACTC-TTCCTGGAGCCCCATTTTCTCTGTGTTCTCTTCTATAAAC----TGGATTTCACC 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1428 ACCCATCCCTGGGGCTTCCTTTGCTCTGCCTTATTTTCAATTGACTGAATGGATCTCACC 1487
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                    1031 ATTOTOCTTTTCACATCTGTCTTGCACATCTGTCTTGCTCATGAGAATTGATATGAAGGA
                                                                                                                                                                                                                                                            1069 ATTTTTTAGTGTTCGTATGAAAGTACAGGGACACGGAGGCCAAGACAGAGTCTAGCAAAGA
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Rattus norvegicus (Norway rat)
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Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harlandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollines, S., Hule, J., Hodgson, A., Hollines, B., Howells, S., Hule, J., Idlebird, D., Jackson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Liu, J., Liu, M., Liu, M., Lebow, H., Levan, J., Lewis, L., Liu, J., Loulseged, H., Lozado, R.J., Lougacre, S., Lopez, J., Marchar, M., Mahindartne, M., Mahmoud, M., Malloy, K., Margum, A., Mancemay, M., Marindas, P., Morris, K., Morris, K., Morris, K., Morris, K., Morris, R., Morris, R., Morris, R., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nawhen, S., Morris, R., Morris, R., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nawokelemeh, O., Okwuon, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasterrak, S., Paul, H., Perez, L., Pranns, E., Pul, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L.-L., Puzc, M., Guiroz, J., Rachlin, E., Reeves, K., Regier, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shelly, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Strong, R., Vorlas, R., Vorlas, R., Vorlas, R., Vorlas, R., Vorlas, R., Vorlas, R., Vorlas, R., Vorlas, R., Vorlas, R., Vorlas, R., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, R., Warren, R., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, R., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J.,
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On Nov 15, 2002 this sequence version replaced gi:23267207.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.imc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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Unpublished
2 (bases I to 246843)
Worley, K.C.
Direct Submission
Submitted (GS-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases I to 246843)
Bat Genome Sequencing Consortium.
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Center clone name: CH200-97B16
Center clone name: CH200-97B16
Assembly program: Phrap; version 0.990329
Consensus quality: 217684 bases at least Q40
Consensus quality: 217884 bases at least Q20
Consensus quality: 220184 bases at least Q20
Estimated insert size: 222530; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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COMMENT

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33607 GGATCATCGAGTTGAAACATCAAGAATGTAGTGTTTTGTACATTAGGTTACAGTAAAAAACA 33666
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TGTATATATTGTGACATCCCTCCATCTCTAGGATGAAACTGAAGTGATCATGATA-GATA
                                                                                    33547 GCAGGGBAAAGTTTATTTACCTTAAACATAAATTGCCGATTCAGAAAATTGGAGATAAGGG
                                                                                                                                                                                                                                                                                            GAATCATCCAATTGAAACTCGAAAAATGTAGTGTTTTGTACATTAGGTTACAGAAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 TGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCACAGATGTGTTGAGACATTCG
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                                                                                                                                        ACTITIGGATCTTTTCACTTTTCTATTGCTGTGATGAAACATGACCAAAACTATCTTGG
                                                                                                                                                                                                                  GCCGGGAAAATTTTAATTTATCTTAACATAAATTTCCTATTTAGAAATTGGACAGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 AGAGAAGGAAAAAGGAAGAAAAAGGAAAAAAGGAAGAATGAATTCAACCAAATCGCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agagagagagaaacaaaaaccaaagagagagaaaaaaargaarrcarcraaarcarcrga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCCCACCACACAGAGAGGATGCTTCAAAAACTCCCAAGTGCTCTCCTGGACGATAGC
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Genes, compositions, kits, and method for identification.
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Patent: WO 0170979-A 21733 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Mammalia; Eutheria; Primatee; Catarrhini; Hominidae;
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CQ414662

    .2143
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                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
  Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1951 CC----ATAGCCTCTCGGCAACCACATCCCATACTCCACCTGCTCCAGCAGGGAACAATA
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                                                                                                                                                                                                                            32891: contig of 32891 bp in length 32991: gap of unknown length 241925: contig of 208934 bp in length 242025: gap of unknown length 243103: contig of 1278 bp in length 243403: gap of unknown length 24454: contig of 1051 bp in length 244554: gap of unknown length 244554: gap of unknown length 246843: contig of 2289 bp in length.
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SILSFWDVGEPNNIATLEDCATMRDSSNPRQWMNDVTCFLNYFRICEMVGINPLNKGKS
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       1491 TTTGTATCTATTGCTCAGCTAGGACCCGAGTCCAATAGTCAATTT-ATTCTAAGCGAACA 1549
                                                                                                                                                                     PRI 10-NOV-1999
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Direct Submission
Direct Submission
Submitted (09-MAR-1999) Shizuo Akira, Osaka University, Department
of Host Defense, Research Institute for Microbial Diseases; 3-1
Yamada-oka, Suita, Osaka 565-0871, Japan
(E-mail:sakira@biken.osaka-u.ac.jp, Tel:81-6-6879-8303,
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                 Matsumoto,M., Tanaka,T., Kaisho,T., Sanjo,H., Copeland,N.G.,
Gilbert,D.J., Jenkins,N.A. and Akira,S.
A movel LpS-inducible C-type lectin is a transcriptional target (NF-IL6 in macrophages
J. Immunol. 163 (9), 5039-5048 (1999)
                                                                                                                                                                   AB024718 2143 bp mRNA linear PRI 10-NOV-1
Homo sapiens mRNA for macrophage C-type lectin Mincle, complete
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.larity 62.3%; Pred. No. 3.9e-86;
Conservative 0; Mismatches 488; Indels
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Homo sapiens (human)
Homo sapiens
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                                           1466 TTCATGTTCACATTTTTCTGTCTCAGGAC
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/gene="Mincle"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buct, T., Max, S.I., Wang, J., Heich, K.,
Hopkins, R.F., Jordan, H., Mooret, T., Max, S.I., Wang, J., Heich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Moreran, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skallaka, U., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skallaka, U., Smallus, D.E.,
Schnerch, A., Schein, J. E., Jones, S.J. and Marra, M.A.
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Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 9, mRNA (cDNA clone MGC:1246 INARE:3507103), complete cds.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 927)
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Submitted (15-NO-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
CCTTCTTAGGGAAGGCCATGCCAGCCATCAGCTCCAAACAGGCTGTAACCAAGTCCACCC
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Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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On Aug 19, 2003 this sequence version replaced gi:l2653848.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Homo sapiens
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                                                                                                                                                                                                          ATGCATGAAGAAGAACAAGAGTGAATGTAATAACAACCAAAATCCAACATAAGAAAATAT 858
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                     824 IGCGCIGAACTICAAAGGACTICATAAGTATITGITACTICATATAAAATA 880
AGAGAGAGAGAAAAACCAAAGAGAGAGAGAAAAAATGAATTCATCTAAATCATCTGA
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Membrane associated proteins
Patent: WO 0112.654 40 22-FEB-2001;
Incyte Genomics, Inc. (US)
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Pred. No. 6.8e-83;
0; Mismatches 215; Indels
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    .968
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Sequence 40 from Patent WO0112662.
AX083498
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 7 Row: 1 Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7657332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIGCTACAATTATGGATCAGGTTCAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTT
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/clone="MGC:1246 IMAGE:3507103"
/tissue_type="Kidney, renal cell adenocarcinoma"
/clone lib="NHH MGC" 14"
/lab_host="DH10B-R"
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/protein id=mAH60015.1"
/db xref="GI:1265349"
/db_xref="LocusID:26253"
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(C12P21/02,C12R1:645), C12N15/00, C12N5/00

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                                                                                                                                                                                                                                                     JEAN YUAN
C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21,
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60/064148 PR
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1. .997
/organism='Homo sapiens (human)'.
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Pred. No. 1.5e-82;
0; Mismatches 216;
                    60/063870,03-NOV-1997 U
60/064809,12-NOV-1997 U
60/065846,18-NOV-1997 U
60/066120,21-NOV-1997 U
60/066770,24-NOV-1997 U
60/066770,24-NOV-1997 U
60/066453,25-NOV-1997 U
1351IN L GURNEY,AUDREY GOD
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                         AUSTIN
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Best Local Similarity 72.9%;
Matches 610; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BD172543.1 GI:28413845
JP 2002223786-A/316.
Homo sapiens (human)
Homo sapiens
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Mincle, C-type lectin; antinflammatory, macrophage, inflammation; disorder, nuclear factor interleukin 6; NP-IL6; ss.
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IL6). Mincle is a macrophage activating protein which can be used in the treatment of immune disorders, and inflammation. Compositions containing the protein have immunomodulatory and antiinflammatory activity. The present sequence represents murine cDNA encoding Mincle
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Best Local Similarity 99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                 TGTACATTAGGTTACAGAAAACAACTTTAGCCACAAAAATAAAGTAATAAACTATT 2517
                                               TGCTATCTCTTCTGTATCCCTAGAATCTCTAGGAGCTTCATATAAAAGATTCGAATTC
                                                                              CATCAAAGGGCACACAAAAGAAATCACAAAGACCATGTGGTTTCTGTCCTTGGGTTTATTT
                                                                                                              AAACATGACCCGAAAACTATCTTGGGCCGGGAAAATTTTAAATTTATCTTAACATAAATTTC
                                                                                                                                                                                                            TGCTATCTCTTCTGTATCCCTAGAATCTCTAGGAGCTTCATAAAAGATTCTGAATTC
                                                                    CATCAAAGGGCACACAAAGAAATCACAAAGACCATGTGGGTTTCTGTCCTTGGGTTTATTT
                                                                                                    GCAAGGTTCATTACACTCCTTGACTTGTATATTGTGACATCCCTCCATCTCTAGGATG
                                                                                                                                    AAACTGAAGTGATCATGATAGATAACTTTTGGATCTTTTCACTTTTCTATTGCTGTGATG
                                                                                                                                                                   AAACATGACCCAAAACTATCTTGGGCCGGGAAAATTTTAATTTAACTTAACATAAATTTC
                                                                                                                                                                                                                                                                                                                                                          Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 21733; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                          Human ovarian cancer DNA marker #21733
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25-MAY-2000;
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The invention relates to nucleic acid markers which are overexpressed in coarain cancer cells as compared to their expression in normal (i.e. noncarous) ovarian cancer cells. The invention also relates to polypeptides cancer antibodise that selectivaly bind to the conceded by the markers, antibodise that selectivaly bind to the confidence of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer which involves comparing the expression of the marker in a patient ample and a normal level of expression of the care corresponds to a secreted protein or a difference between the expression levels inflates ovarian cancer. The level of expression of the marker is detected using an antibody that specifically binds with the fragment corresponds to a secreted protein or to a transcribed polymuclectide or its portion. The level of expression of the marker is assessed by detecting the presence of protein or protein fragment corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed protein or protein fragment. Alternatively, the level of expression of the marker is a sessessed by detecting the presence of a transcribed or the polymuclectide or mitching the marker, under stranger. Conditions. The polymuclectide or mitching expression of the marker is a subsequent time and comparing the level of expression of the marker is a language as a first point in time, repeating the method is earlied out time and comparing the level of expression of the marker in a pubged or antibody of the invention is used to trast ovarian cancer in polypeptide or antibody of the invention and protein or protein become a limit and the sequence at

267 CAGCTCTCAAA---TTTCCGGGGGGAACTTACAGCCACATAGAAATATTAAGGAGCTTTC 323

324 CHILLILCHANACAIGHGAIGNANACAILL CAGCIACHGANACAILL CAGAGACAITH 313
324 CHGCHACAGGAACATTA 383
352 CHGCHACAATTATGGATCAGGTTCAGGAATTTGTTGTTGTTGTACTGGAACATTA 383
352 CHGCHACAATTATGGATCAGGTTCAGTAAAAATTGTTGTTGTTGTTGTTGAACTTGAACATATTT 411

(first entry)

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RESULT 3 ADO24494 AD024494

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The present invention describes an isolated human PRO polypeptide (I).

Also described: (I) an isolated PRO nucleic (II) acid encoding (II); (2) a vector (III); (3) a host cell (IV) comprising (III); (4) producing (I); (5) a chimeric molecule (V) comprising (II); (4) broducing (I); (5) a chimeric molecule (V) comprising (I) in the decrease (C) in an antagonist of (I), or (VI) in compliation with a carrier; (8) composition of matter comprising (I), an agonist of (I), an antagonist of (I), or the antibody (VI); (9) (1), an agonist of (I), an antagonist of (I), or the antibody (VI); (9) (1), an agonist of (I), an antagonist of (I), or the antibody (VI); (9) (1), an agonist of (I), an antagonist of (I), or the antibody (VI); (9) (1), an agonist of (I), an antagonist of (I), or the antibody (VI); (9) (1), and (II) identifying a compound that inhibits to expression of a gene encoding (I); (I2) identifying a compound that inhibits the activity of (I); (II) identifying a compound that inhibits the activity of (I); (II) identifying a compound that inhibits the activity of (I); and (I2) stimulating the immune response in mammal. (II) has mammal and a compound that inhibits the activity of (I); and (I2) stimulating the immune response in a mammal. (II) is useful for its antagonist to the mammal. (II) is useful for treating an immune related disease in a mammal. (II) is useful for treating an immune related disease in a mammal. (II) is useful for treating mammal having an immune cological, interpolate in a mammal. (II) is useful for treating mammal having an immune related disease in a mammal. (II) is useful for treating mammal having an immune systemic systemic vascultis, osteoathritis, composition, systemic slerosis, idiopathic inflammatory and indicated systemic leaves or immune-mediated skin diseases in indicated systemic systemic cological, indiopathic indicated in an antoimmune parenches and numan PRO protein
                                                                                                                antianaemic; antiarthritic; antiinflammatory; antipsoriatic;
                                                                                                                                                                                                                               spondyloarthropathy; systemic sclerosis; idiopathic inflammatory myopathy; Sjogren's syndrome; systemic vasculities sarcoidosis; autoimmune haemolytic anaemia; sutoimmune disease; immune-mediated skin disease; bullous skin disease; erythema multiforme; context dermatitis; psoriasis; lymphadenopathy; splenomegaly; leukopaenia; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated PRO polypeptide e.g. PRO37544, PRO69493, PRO87327 etc, capable of stimulating an immune response, useful for treating diseases such as rheumatoid arthritis, psoriasis, and leukopenia.
                                                                                                                                                                                     ostecarthritis;
                                                                                                                                  antirheumatic; dermatological; immunostimulant; immunosuppressive; osteopathic; vasotropic; immune related disease; inflammatory immune response; rheumatoid arthritis; osteoarthritis juvenile chronic arthritis; systemic lupus erythematosus;
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                                                                  Human PRO244 encoding cDNA SEQ ID NO:133.
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Best Local Similarity 62.3%; Pred. No. 5.7e-98;
Matches 915; Conservative 0; Mismatches 488; Indels
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                                      AAF81741 to AAF81777 encode the human membrane associated proteins (MEMAP) given in AAB74695 to AAB74731. MEMAPS have cytostatic, antidiarmatory, anticonvollabant, immunosuppressive, antidiarneic and antidonvollabant, immunosuppressive, antidiarneic and antidiarneic and antidiarneic activities, which can be used in gene therapy.

MEMAPs and agonist of MEMAPs can be used to treat a disease or condition associated with decreased expression of functional MEMAP and antidonists of MEMAP are used to treat a disease or condition associated with coverexpression of functional MEMAP. These disorders include cell coverexpression of functional MEMAP. These disorders and gastrointestinal disorders. The MEMAP polyvucleotides and proteins are also used for the disorders. Inflammation, atherosclerosis, epilepsy and diarrhoea. MEMAP proteins can be used to screen for compounds which specifically bind MEMAP proteins and used to screen for compounds which small can be studied to provide information concerning human disease. Anti-MEMAP antibodies are useful in immunoassays for the canimals which can be studied to provide information concerning human disease. Anti-MEMAP antibodies are useful in immunoassays for the canimals which associated with MEMAP. Polymucleotides encoding MEMAP can be delivered to target calls with genetic abnormalities with respect con be delivered to target cells with genetic abnormalities with tespect and when the expression of MEMAP to treat or prevent a disorder associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 968;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 968 BP; 314 A; 197 C; 205 G; 252 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 441; DB 4; Length 96
Pred. No. 1.8e-94;
0; Mismatches 215; Indels
               Page 151; 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 73.0%;
Matches 611; Conservative
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The present invention relates to hepatic-fibrosis disease markers haftpedisty-bapsols); and related proteins (ABF9063-ABF90917). The ABF9063-ABF90917). The reading hepatic fibrosis caused sequences are useful for detecting and treating hepatic fibrosis caused by alcohol consumption, virus infection, etc., and the associated chronic bepatities, etc. leading to liver cirrhosis and hepatic actionan. The markers allow the cause of hepatic fibrosis to be clarified (diagnostic precision), so more suitable treatments can be developed and given.
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CCCAAGGCAAAATTGGAATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAAT 781
                                                                                                                                                        GGTAGGAATAAATCCTTTGAACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACTCAA 841
                                                                                                                                                                                                                     ATGCATGAAGAAGAACAAGAGTGAATGTAATAACAACCAAAATCCAACATAAGAAAATAT 858
                                                                                                                                                                                                                                                                              antibodies, useful for improved diagnosis, screening and developing drugs to treat hepatitis, to control cirrhosis and carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACACAATGCACAGAGGAGGATGCTTC---TCTTCCCAAATGTTCTTATGGACTGTTGC 241
                                                                                                                                                                                                                                                                                                                                                                                                       CGGGGCCTCCATCCTGTTTCTCAGTGGCTGTTTCATCACCAGATGTGTCGTAAATGG
                                                                                                  GCCAGAAATAAGTCCTCAGGACTAAGTGCAA-----GGAAATACAAGGGACATGGCTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chronic hepatitis; liver cirrhosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatic fibrosis disease markers comprising polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 1.8e-94;
0; Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  marker SEQ ID 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human hepatic-fibrosis disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-2002; 2002JP-00065013.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADF90738 standard; DNA; 976
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TGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTCG 301
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                                     CAGCTCTCAAA - - - TTTCCGGGCAGAACTTACAGCCACATAGAAATATTAAGGAGCTTTC
                                                                                                                                                     CTGCTACAATTATGGATCAGGTCAGTCAGAATTGTTGTCCATTGAACTGGGAATATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            584 CTCCAGGAAGAACTGGAATGATAATCCCTGTTTCTACAGTATGCCTTGGATTTGTGAGAT 743
                                                                                                                                                                                                                                                                                                                            The invention relates to 167 novel human CD (cluster of differentiation) like molecules (ADR41388-ADR41563) and to CDNAs encoding them (seqid:11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCCCACCACACAGAGAGGATGCTTCAAAAACTCCCAAGTGCTCTCCTGGACGATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGGCCTCCATCCTGTTTCTCAGTGGCTGTTTCATCACCAGATGTGTCGTAACATATCG
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 990 BP; 342 A; 192 C; 206 G; 249 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 99; 1243pp; English.
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                                                                                25-SEP-2001; 2001WO-US029838
                                                                                                             26-SEP-2000; 2000US-0235484P
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similaricy
nes 611; Conservative
                                                                                                                                        (HUMA-) HUMAN GENOME
                                                                                                                                                                                              WPI; 2002-405050/43.
P-PSDB; ADR41476.
                                                                                                                                                                   Rosen CA, Birse CE,
                           WO200226930-A2
 Homo sapiens.
                                                       04-APR-2002
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CAGCICICAAA---ITICCGGGCAGAACTIACAGCCACAIAGAAAIATAAGGAGCITIC
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        9705-0063735P.
9705-0063738P.
9705-0064215P.
9705-0064103P.
9705-0064809P.
9705-0064809P.
                                                                                   97US-0065693P.
97US-0066120P.
97US-0066364P.
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97US-0066466P.
97US-0066511P.
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97US-0066772P
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                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                                                                                                                                                               P-PSDB; AAY13403
        29-OCT-1997;
29-OCT-1997;
31-OCT-1997;
31-OCT-1997;
03-NOV-1997;
07-NOV-1997;
                                                                                   18-NOV-1997;
21-NOV-1997;
21-NOV-1997;
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25-NOV-1997;
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GCCAGAAATAAGTCCTCAGGACTAAGTGCAA-----GGAAATACAAGGGACATGGCTTAC 798
                                                           ATGCATGAAGAAGAACAAGAGTGAATGTAATAACAACCAAAATCCAACATAAGAAAATAT 858
                                          769 GGTAGGAATAAATCCTTTGAACAAAGGAAAATCTCTTTAAGAACAAGAGGCACAACTCAA 828
                                                                           Secreted protein; transmembrane protein; human; enterocolitis; Callinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; parkinson; disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair; ss.
                                                                                           CTATCAGGCATCAGAAGGACTGCACATGTATCATTACTGGGACATAAGTAAAAAGA 915
                                                                                                            Protein PRO244 cDNA clone DNA35668-1171.
                                                                                                                                                     AAX52274 standard; DNA; 997 BP
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97US-0059113P.
97US-0059113P.
97US-0059121P.
97US-0059122P.
97US-0059122P.
97US-0059283P.
97US-0062287P.
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97US-0063704P.
97US-0063732P.
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17-0CT-1997;
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AXX52213-74 encode secreted and transmembrane human proteins, and are obtained from cDNA libraries prepared from fetal lung, fetal kidney, cletal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO21 and PRO217 can be used for disorders associated with the preservation and maintenance of gastroinestinal mucosa and the repair of scute and chronic mucosal lesions (e.g. entercollists, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus arrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the ulseases related to growth or survival of nerve cells including PRO255 can be used as for fibromodulin, e.g. for reducing dermal scring, PRO264 can be used as a target for anti-tumor drugs PRO533 may be used as an anti-thrombotic agent; PRO287 polypeptides and portions may be used as an anti-thrombotic agent; PRO287 polypeptides and portions may be used for treating problems of the kidney, uterus, endometrium, can be used for treating problems of the kidney, uterus, endometrium, can be used for treating problems of the kidney, uterus, endometrium, can be used for related tissue, e.g. in the heart of genital tract
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                                                                                                                                                                                                                 New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration.
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Yuan
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Pennica D,
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16-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflamatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; vasotropic; chemotaxic; angiogenic; neuroprotective; vasotropic; chemotaxic; angiogenic; antiarthritic; antirheumatic; antiarthritic; antirheumatic; antiarthritic; antirheumatic; thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease; Alzhaimer's, ALS; neuropathy; dermal scarring; wound healing; nerve repair; thrombosis; bone; cartilage formation; angiogenesis; asthma; rheumatoid arthritis; multiple scalerosis; inflammatory disorder; diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.
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                                                                                                                                                                                                                                GGGTCAGTGGCAATGGGACGGACGCACCTTTGACAAAGTCTCTGAGCTTCTGGGGATGT
                                                                                                                                                                                                                                                                              606 AGGGGGCCCAACAACATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAA
                      CTGCTACAGTGAGGCATCAGGTTCAGTCAAGAATTGCTGTCCTTTGAACTGGAAACATTA
                                                                     TCAATCTAGTTGTTATTTTTTCTCTACGACAACCTTGACCTGGTCATCAAGTTTAAAGAA
                                                                                           rcaarccaecrecracircrirricracreacaccarriccreecerraacriraaacaa
                                                                                                                     TTGCTCAGACATGGGGGCTCACCTGGTGGTTATCGACACACAGAAGAGCAGGAATTCCT
                                                                                                                                    CTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCT
                                                                                                                                                                   TTTTCGCACAAAATCTAAAAGGAAAGAGTTTTATATTGGACTGACAGACCAGGTGGTGGA
                                                                                                                                                                                      TTCCTACAAGAAACCTAAAATGAGAGAGTTTTTTATTGGACTGTCAGACCAGGTTGTCGA
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The invention relates to a novel nucleic acid encoding a PRO polypeptide. The polypeptides and polynuclectides of the invention may be useful as research tools and as therapeutics for treating enterocolitis, Zollinger-Bilson syndrome, gastrointestinal ulceration, psoriasis, cancer, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal scarring and wound healing, nerve repair, thrombosis, bone and/or cartilage formation, anglogenesis, asthma, rheumatoid arthritis, multiple sclerosis, inflammatory disorders, atherosclerosis, cardiac injury, infertility, premature aging, AIDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.
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Hillan KJ, I
Stewart TA,
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                                                                                                                                                                                                                                                                                                                                                                     ВР
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99US-0146222P.
99WO-US020594.
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99WO-US028313
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99WO-US023089
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Godowski PJ, G
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05-OCT-1999;
29-NOV-1999;
30-NOV-1999;
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28-JUL-1999;
08-SEP-1999;
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20-DEC-1999;
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GGTAGGAATAAATCCTTTGAACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACTCAA 785
                                                                                                                                                                                                                       The present sequence is one of sixty one nucleic acids encoding novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzhaimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infortility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carcirricaaaccrereareaeaaaaerrrcaecraccreaeaarrrcacaeaecrere
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carcinoma) and neurodegenerative diseases (e.g. Alzheimer'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.5%; Score 439.4; DB 4; Length 997; 72.9%; Pred. No. 4.3e-94; tive 0; Mismatches 216; Indels 11.
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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
                   859 CTATCAGGCATCAGAAGGACTGCACATGTATGTATTACTGGGACATAAGTAAAAAGA 915
                           TGCGCTGAACTTCAAAGGACTTCATAAGTATTTGTTACTCTGATACAATAAAAATA 902
                                                                                                   Human DNA encoding PRO polypeptide sequence #12.
                                                              AAS45936 standard; cDNA; 997 BP
                                                                                                                                                                                                                                                                  2000US-0191314P.
2000US-0192655P.
2000US-0193032P.
2000US-0193053P.
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2000US-0194449P.
2000US-01954647P.
2000US-0195600P.
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2000US-0196820P.
2000US-0198121P.
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2000US-0187202P,
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11-APR-2000;
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                                                                                                                                        PCR primer.
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primers PAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of comparing the level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, bigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human contacted with it. A specific polypeptide can be used to stimulate the proliferation of differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also canceptablibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or the PRO nucleic acide can be used for genetic analysis of individuals with genetic disorders
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                                                                                                                                                                                     Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and screen for modulators of the compounds.
   Gurney AL;
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, Goddard A, Godowski PJ,
Wood WI, Zhang Z;
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o, Chen J, Desnoyers L, Smith V, Watanabe CK,
                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 23; 774pp; English.
                                                                                            WPI; 2001-602746/68.
P-PSDB; AAU29035.
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                                Pan J,
      Baker
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563 623 605

504 486 564 624 TGGGGAGCCCAACAATATAGTTTTGGTGGAGGACTGTGCCACCATAAGGGACTCTTCAAA 683

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The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a PRO protein extracellular domain. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, producing a PRO polypeptide (by culturing the host cell for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture), an isolated PRO polypeptide (having at least 80% sequence identity to: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, in generating probes and in tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
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          970S-0063738P-
970S-0064215P-
970S-0064103P-
970S-0064248P-
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970S-006631P-
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24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
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30-MAR-2000; 2000WO-US008439
22-MAY-2000; 2000WO-US014042
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24-AUG-2000; 2000WO-US023328
18-SEP-2000; 2000US-00665350
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Filvaroff E, Fong S, G
Godowski PJ, Grimaldi J
Mather JP, Pan J, Paor
Williams PM, Wood Wi,
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P-PSDB; ABU71950.
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  606 AGGGGGCCCAACAAACATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAA 665
                                                 GCCAGAAATAAGTCCTCAGGACTAAGTGCAA-----GGAAATACAAGGGACATGGCTTAC 798
                                                                                                       GGTÄGGÄÄTÄÄÄTÄCTTTGAÄCAÄÄGGAÄÄTCTCTTTÄÄGAÄCÄGAÄGÄCÄCAACTCÄA 785
                                                                                                                              ATGCATGAAGAAGAACAAGAGTGAATGTAATAACAACCAAAAATCCAACATAAGAAAATAT 858
                                                                                                                                                                           859 CTATCAGGCATCAGAAGGACTGCACATGTATGTATTACTGGGACATAAGTAAAAAGA 915
                                                                                                                                                                                        846 TGCGCTGAACTTCAAAGGACTTCATAAGTATTTGTTACTCTGATACAAATAAAAATA 902
                                    CTCCAGGAAGAACTGGAATGATAATCCCTGTTTCTACAGTATGCCTTGGATTTGTGAGAT
                                                                                                                                                                                                                                                                                                                                                    Human; 88; gene; secreted protein; transmembrane protein; PRO; gene therapy; chromosome identification; chromosome marker.
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acid sequence encoded by a nucleic acid molecule deposited with an ATCC acid sequence encoded by a nucleic acid molecule deposited with an ATCC unuber (detailed in the specification); or (c) an extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking its associated signal peptide), a chimaeric molecule comprising a PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting a PRO245 or PRO1868 in a sample suspected of containing the polypeptide, clinking a bioactive molecule to a cell expressing a PRO245 or PRO1868 uncleic acids which encode PRO and be used to generate either transgenic animals or knock-out animals which may be used in the crimals and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue or properties and nucleic acids may also be used in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sequences. The present sequence encodes a PRO protein
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726 GGTAGGAATAAATCCTTTGAACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACTCAA 785
                      799 ATGCATGAAGAAGAACAAGAGTGAATGTAATAACAACCAAAAATCCAACATAAGAAAATAT 858
                                             786 ATGTGTAAAGAAGGAAGAGCAAGAACATGGCCACACCCACGCCCCACACACGAGAATTTG 845
                                                                                                                                                                                                                                                                 chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast, prostate; rectal; cervical; liver; cancer; TNF-alpha; tumour necrosis factor-alpha; proliferation; differentiation; chondrocyte cell; bone disorder; cartilage disorder; sports injury; arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;
                                                                     859 CTATCAGGCATCAGAAGGACTGCACATGTATGTATTACTGGGACATAAGTAAAAGA 915
                                                                                            846 TGCGCTGAACTTCAAAGGACTTCATAAGTATTTGTTACTCTGATACAATAAAATA 902
                                                                                                                                                                                                                                                       Human; PRO polypeptide; secreted protein; transmembrane protein;
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323
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07-DEC-1998;
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                                                                                               Three hundred and five nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, and for detecting the presence of tumor in a mammal.
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      Gurney AL;
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   Goddard A, Godowski PJ,
ood WI, Zhang Z;
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                  Watanabe CK,
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P, Chen J,
Smith V, W
                                                                   P-PSDB; ABU86204
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tumour necrosis factor alpha, chondrocyte cell; tumour, gene therapy,
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99WO-US010733.
99WO-US012252.
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in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoresis purposes, for chromosome identification, as chromosome markers, as therapeutic agents, for stimulating the release of TNF-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyces and detecting the presence of a tumour. The PRO polypeptides and nucleic acids may also be used diagnostically for tissue typing. The sequences presented in ACADS-O-ACADSOOG are the cDNAs encoding the PRO
                                                                                                                                                                                                                                                                                                                    186 researcccearccarrrcreserscersirrearcaceasarsrersfeararrrcs 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotide sequences. The nucleotide sequences are useful as probes,
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                                                                                                                                                                                                                               Length 997;
                                                                                                                                                                                                Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;
                                                                                                                                                                                                                            Score 439.4; DB 8; Length
Pred. No. 4.3e-94;
0; Mismatches 216; Indels
                                                                                                                                                                 polypeptides of the invention
                                                                                                                                                                                                                            17.5%;
                                                                                                                                                                                                                                                         Matches 610; Conservative
                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the proliferation or differentiation of chondrocyce calls by contacting the cells with a PRO polypeptide, a method for detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the

    secreted and transmembrane PRO polypeptides and nucleic acids, usef
gene therapy, in chromosome and gene mapping, as chromosome markers,
tissue typing, and in chromosome identification.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 23; 706pp; English
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2000US-00665350
2000US-00709238
2000WO-US0330572
2000WO-US0332678
2000US-00747259
2000WS-00334956
2001WS-00806520
2001US-00816744
99US-00380142.
99WO-US020111.
99WS-00403297.
99WS-00403284.
99WO-US028301.
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2000WO-US020710.
2000US-00644848.
2000WO-US023328.
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2001US-00854280
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2001WO-US017800.
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2001WO-US019692.
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2001US-00908827
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2001US-00924419
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                                                                                                                     2000WO-US
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28-JUL-2000;
22-JUG-2000;
24-AUG-2000;
18-SEP-2000;
18-SEP-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-2001; 2
06-AUG-2001; 2
13-AUG-2001; 3
25-AUG-1999;
01-SEP-1999;
15-SEP-1999;
18-OCT-1999;
12-NOV-1999;
01-DEC-1999;
30-DEC-1999;
05-JAN-2000;
18-FEB-2000;
22-FEB-2000;
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17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
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22-MAR-2001;
10-MAY-2001;
10-MAY-2001;
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01-JUN-2001;
05-JUN-2001;
20-JUN-2001;
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09-JUL-2001;
18-JUL-2001;
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01-MAR-2000;
02-MAR-2000;
15-MAR-2000;
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-DEC-2000;
-DEC-2000;
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AACACAATGCACAGAGGAGGATGCTTC---TCTTCCCAAATGTTCTTATGGACTGTTGC 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane). Methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of tumours, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumours. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human CDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence represents a CDNA encoding a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                      transmembrane
                                                                                                                                                                                                                                                                                                     Three hundred and five nucleic acids encoding secreted and transmembrand PRO polypeptides, useful for the diagnosis, prevention and/or treatment of tumors, such as adrenal, lung, colon, breast, prostate, rectal,
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                                                                                                                                                                                                                                Godowaki PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;
                                                                                                                                                                                                                               L, Goddard A, Go
Wood WI, Zhang
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                                05-UN-2001; 2001W3-00874503.

20-JUN-2001; 2001W0-US019692.

29-JUN-2001; 2001W0-US021066.

09-JUL-2001; 2001W3-00908827.

18-JUL-2001; 2001W3-00908827.

30-JUL-2001; 2001W3-00918595.

06-AUG-2001; 2001W3-00941992.

18-AUG-2001; 2001W3-00941992.

28-AUG-2001; 2001W3-00941992.

29-AUG-2001; 2001W3-00941992.

29-AUG-2001; 2001W3-00941992.

15-AUG-2001; 2001W3-00941992.
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Watanabe CK,
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nilarity 72.9%;
Conservative (
            2001US-00866028
2001WO-US017800
                                                                                                                                                                                                                                                                                                                                          cervical or liver tumors.
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P-PSDB; ABU80445.
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ses 610; Conserv
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                                                                                                                                                        tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
846 TGCGCTGAACTTCAAAGGACTTCATAAGTATTTGTTACTCTGATACAAATAAAATA 902
                                                                                                                                 cDNA encoding human PRO protein #12.
                                                                                                                                                                     PRO; gene therapy; gene; ss.
                                                            ACA66545 standard; cDNA; 997 BP
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99US-00403297.
99US-00423844.
99WO-USO28301.
99WO-USO28551.
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98US-00168978.
98WO-US021141.
98WS-00187368.
98WS-0020554.
99WS-0020554.
99WS-0020558.
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99US-00380137.
99US-00380138.
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2000US-00644848.
2000WO-US023328.
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2000US-00665350.
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2000WO-US008439
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18-SEP-1999;
18-OCT-1999;
12-NOV-1999;
01-DEC-1999;
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05-JAN-2000;
18-FEB-2000;
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24-FEB-2000;
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28-JUL-2000;
22-AUG-2000;
24-AUG-2000;
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10-MAY-2001;
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01-DEC-1998;
07-DEC-1998;
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02-JUN-1999;
25-AUG-1999;
25-AUG-1999;
25-AUG-1999;
25-AUG-1999;
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                                                                                   ACA66545;
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model	Run on: June 9, 2005, 03:48:21; Search time 8065 Seconds (without alignments) 11879.450 Million cell updates/sec	Title: Perfect score: 2517 Sequence: 1 cggtctgttactcttgaactaaataaagtaataaactatt 2517	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 34239544 seqs, 19032134700 residues	Total number of hits satisfying chosen parameters: 68479088	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	ST:* gb_est1:* gb_est2:* gb_hrc:*	4: 92-est3:* 5: 92-est4:* 6: 92-est5:* 7: 92-est6:*	gb_gss1:* gb_gss2:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description	1991 79.1 2233 3 AK089286 AK089286 MU 1338 53.2 4017 3 AK036493 AK036493 AK036493 MU	918.6 36.5 80.9 9 EANDSIGN EANDSIGN EANDSIGN TO CO. 28.1 731 4 BGO67349 BG067349 BY761232 BY761232	665.6 26.4 705 6 BY764212 BY764212 BY 655.2 26.0 701 6 BY763813 BY763813 BY 650.0 26 0 71 6 BY763813 BY763813 BY	650.4 25.8 71 9 CRO71785 CRO71785 BY744630 BY744630 BY	637.8 25.3 666 6 BY747821 BY747821 BY 635.6 25.3 655 6 BY749084 BY749084 BY749084 BY 628.2 25.0 644 4 BG080418 BG080418 H3	625.4 24.8 645 6 BY743467 BY743467 BY 623.4 24.8 731 2 BE292591 BE292591 60	17 602 23.9 667 6 BY147840 BY747840 BY747840 18 594 23.6 660 2 BE292395 BE292395 601057892 19 581.2 23.1 728 6 BY742764 BY742764 BY742764	530.2 21.1 647 6 BY763796 BY763796 BY 528 21.0 548 7 CK329780 CK328780 HB	497.6 19.8 671 6 BY74948B BX 484.8 19.3 570 5 BP771395 BP771395 BF 484.4 19.2 486 5 BX516799

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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Loature 420, 563-573 (2002) E (bases 1 to 2233) S Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W., Hori, F., Imotani, K., Ishii, Y., Itoh, W., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Sakai, C., Sakai, K., Sakzume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagaum, M., Tagawa, A., Takahani, R., Tanaka, T., Towar, T., Yasunishi, A., Tanaka, T., Towar, T., Yasunishi, A.,	Muramatsu, M. and Hayashizaki, Y. Direct Submission Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Taurumi-ku, Yokohama Kanagawa 230-0045, Japan (8-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,	Fax:81-45-503-9216) Fax:81-45-503-9216) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/RRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. Figure Phense Additional Additional Cambridge and Cambr	URL:http://fantom.gsc.riken.jb/. Location/Qualiflers 1. 2233 /organism="Mus musculus" /mol_type="mRNA" /strain="c57NIG0" /db_xref="raxon.10090" /db_xref="raxon.10090" /db_xref="taxon.10090" /db_xref="taxon.10090" /clone="f730001C01" /cell_type="Be-derived CD11 +ve dendritic cells" /clone="f73001C01" /cell_type="Be-derived CD11 +ve dendritic cells" /clone="f73001C01" /cell_type="Be-derived CD11 +ve dendritic cells" /clone="f73001C01" /cell_type="f73001C01"	nilarity 9.1%; Score 1991; DB 3; Length 2233. Conservative 0; Mismatches 26; Indels 76 Conservative 0; Mismatches 26; Indels 76 STCTGTTACTCTTGAACTTTTAAAAAGGGCCAAGGATTCACCATTCAACTCTTGAACTTTTAAAAAGGGCCAAGGATTCACCATTCAACTCTTGAACTTTTAAAAAGGGCCAAGGATTCACCATTCAACTTTTAAAAAGGGCCAAGGAATTCACCATTCAACTTTTAAAAAGGGCCAAGGAAGAAGGAAG
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	ACTGCATTTATTGCATGATATTCTGTCAATATAGACCATGTTTCTTCCAGACAAGC 1549 	JOURNAL	Normalization and prepare full-length Genome Res. 10 (10 20499374
<u>~</u> ~	ITAGGAA-CITCAGCAGCAGTCACACATIGIAATAAACAIGIATCCTIGAGTAGGAA 1608 	FUENCE REFERENCE AUTHORS	11042159 3 Shibata, K., Itoh, M Konno, H., Akiyama,
9-9	TAAACTAAATAAATTAATTTGTCATATTAGCACTCATTACGAGCACTTCTATTAGAC 1668 		Sumi, N., ishii, Y., Yamamoto, R., Matsuu Fujiwake, S., Inoue Yoneda, Y., Ishikaw
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4=4	GATTITCCTCCCAAITICAIGIGCTCCTCTTIGITTIAAACCCACTCTATCIGCTC 1908 	TITLE	ine FANIOM Consort Group Phase I & II Analysis of the moi of 60,770 full-len
	GCTTCCTGAATGCACTTGAGTATAAGGCTTTCTACTGGACCATAGCCTCTGGCAAC 1968 	JOURNAL REFERENCE AUTHORS	Nature 420, 563-5 6 (bases 1 to 40 Adachi,J., Alzawa Fukuda,S., Furuno
CACATO	ATCCATACTCCACTGCTGCAGGGAACAATAGCCAATTGACCATCTTCAGCTG 2028 		Hayashida, K., Haya Hori, F., Imotani, K Katoh, H., Kawai, J. Koya, S., Kurihara,
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5=5	TTCTGAATTCC 2161 TTCTGAATTCC 2233		Physical and Chemic Exploration Resear RIKEN Yokohama Inst Kanagawa 230-0045,
		COMMENT	URL:http://genome.gravial-15-503-9216 cDNA library was p

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Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830118H07 product:C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9, full ak036493

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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Onkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-5EB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
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                                                                                                                                                                                                                                                                                                                      Score 1338; DB 3;
Pred. No. 1.9e-313;
0; Mismatches 15;
                               /organism="Mus musculus"
/mol type="mRNA"
/mol type="mRNA"
/db strain="CSTBL/6J"
/db xref="FANTOM DB:9830118H07"
/db xref="taxon:10090"
/clone="9830118H07"
Location/Qualifiers
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Best Local Similarity 98.8%;
Matches 1369; Conservative
                                                                                                                                             /sex="male"
                                                                                                                                                                                                                 misc_feature
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Rodentia; Sciurognathi, Muzidae; Muzinae; Mus. 1 (Dases 1 to 731)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Garbovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H. III. Becker,K.G. and Ko,M.S.H. Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                 Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                   10922068
KEYWORDS
SOURCE
ORGANISM
                                                                           REFERENCE
AUTHORS
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MEDLINE
PUBMED
COMMENT
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                                                                          1337 GATCTAGTCCACTCTTCCTGGAGCCCCATTTTCTCTGTGTTCTCTTCTATAAACTGGATT
                                                                                              GATCTACTCCACTCTTCCTGGAGCCCCATTTTCTCTGTGTTCTCTTTTAAACTGGATT
                                               Gaps
                                             7
                  Length 865;
                                               11; Indels
               32.5%; Score 818.6; DB 9; 98.5%; Pred. No. 1.3e-187; ive 0; Mismatches 11;
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                                            Matches 846; Conservative
                               Similarity
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/lan_note="Varior bills" // Jan_note="Vector: pSPORT; Site_1: Sal1; Site_2: NotI; This clone is among a rearrayed set of 15.247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profilling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. US A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7:5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
Or Jan 26, 2001 this sequence version replaced gi:12549918.
Other_ESTS: H3053D08-5
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
33 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3053 row: D column: 08
Seq primer: -21M13 Forward
High quality sequence stop: 731
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/dev_stage="Clones arrayed from a variety of cDNA
libraries"
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28.1%; Score 706.2; DB 4;
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BG067349 T31 bp mRNA linear EST 17-DEC-2003 H3053D08-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3053D08 3', mRNA sequence.
BG067349.2 GI:40014147

BG067349/c LOCUS ACCESSION

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Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watenabe, Y., Walle, C., Wilming, L.G., Wynshaw-Boris, A., Yangsisawa, M., Yang, L., Yang, L., Yang, L., Zavolan, M., Zhu, Y., Zammer, A., Carninci, P., Hayateu, N., Hirozane Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Sakakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishi, Y., Itoh, M., Kagawa, T., Wayazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp/
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Direct Submission
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RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequenced in Mouse Genome
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequenced in Mouse Genome
Encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division mental Animal Research in Riken contributed to
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
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Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistence we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/clone_lib="RIKEN full-length enriched, bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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Best Local Similarity 96.8%; Pred. No. 5.6e-158;
Matches 727; Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'tissue type="bone marrow"
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/clone="G530005P16"
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/strain="C57BL/6J"
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8. Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nixaki,Y., Furuno,M., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yadi,K., Tomatu,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.B., Cousins,S., Dalla,B., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaaterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,B.D., Konagaya,A., Kurochkin,I.V., Lee,Y., Lehhard,B., Loknos,P.A., Maglott,D.R., Maltais,L., Marchionni,L., Mockenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pescole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
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BY761232 RIKEN full-length enriched, bone marrow macrophage Mus
musculus cDNA clone G530005P16 3', mRNA sequence.
                                                 551 AACAGGTAGAAAGCAGATGTCTGTATAAAGAGACTTTAATGGTCACTATGTCATCCTGTT
                                                                                                                                                                                                                                                                                                                                CTTTCTACATCCTTGGCTCTAGCTTATCTATCTATCAGTACATAGATCACTTCTGTGTTC
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BY761232.1 GI:27196760
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="t----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTATCTCTTCTGTATCCCTAGAATCTCTAGGAGCTTCATATAAAAGATTCTGAATTCCA 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2283 ACTGAAGTGATGATGATAGATAAGTTTTTGGATCTTTTTCACTTTTCTATTGCTGTGAA 2342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2403 ATTTAGAAATTGGACAGGTGGGGAATCATCCAATTGAAACTCGAAAAATGTAGTGTTTTG 2462
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                                                                  1804 AACCCATCCTTACTCTCCTCACTACAACCTGCTCCTATCCACCTCACTGATTTTCCCTCC 1863
                                                                                                                                                      CAATTICATGLGCTCCTCTTTGTTTTAAACCCCACTCTATCTGCTCAGTGCTTCCTGAATG 1923
                                                                                                                                                                                                                                                                                                                                                                                                                GAGCTCCATGCCATTCATGCTGGAATTTGGGTTGTTTTATGTAACCTTTATATATTGTG 2102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 TCAAAGGCACACACAAAAAAATCACAAAGACCATGTGGTTTCTCTCCTTGGGTTTATTTGC 485
                                                                                               66 AANCCATCCTTACTCTCCTCACTACAACNTGCTCCTATCCACCTCANTGATTTTCCCTCC 125
                                                                                                                                                                            126 CAAINTCATGTGCTCCTCTTTGTTTTAAACCCACTCTATCTGCTCAGTGCTTCTGAATG 185
                                                                                                                                                                                                                                                              CACTTGAGTATAAAGGCTTTCTACTGGACCATAGCCTCTCGGCAACCACATCCCACACCCCCCC 245
                                                                                                                                                                                                                                                                                                                                                                 246 ACCTGCTCCAGCAGCAACAATAGCCAATTGACCATCCTCAGCTGAGGATGGAATTTCAT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATCTCTTCTGTATCCCTAGAATCTCTAGGAGCTTCATAAAAAGATTCTGAATTCCA 425
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T.,, Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
606 ACATGAGCCAAAACTATCTTGGGCCGGGAAAATTTTAATTTTATCTTAACATAAATTTCCT
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Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Kawaji, H., Kawasawa, Y., Jackson, I.J., Jarvis, B.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Lee, Y., Lee, Y., Lee, Y., Lee, Y., Lee, Y., Lee, Y., Lee, Y., Lee, Y., Lee, Y., Lee, Y., Lee, Y., Lee, Y., Lee, Y., Maglott, D., Nangaya, A.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pescole, G.,
Petrovsky, N., Pillai, R., Pontius, Ju., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Tasadale, R.D., Tomita, M.,
Verado, R., Wagner, L., Wahlestedt, C., Wang, Y., Waranabe, Y.,
Walls, C., Wilming, L.G., Wynshaw, Boris, A., Yanagiaswa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatun, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Alzawa, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebitro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9226
Email: genome-reseges.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi.J., Alzawa.K., Akimura.T., Arakawa.T., Carninci.P.,
Rukda.S., Hashizume, W., Hayashida.K., Hirozane.T., Hori.F.,
Imotani.K., Ishil.Y., Itoh, M., Kagawa.I., Kwawai,J., Kojima.Y.,
Kondo, S., Konno, H., Koya.S., Miyazaki,A., Murata.M., Nakamura.M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission Untert Submission
Computational Analysis of Full-Length Mouse CDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected CDNAs to
prepare full-length CDNA ibraries for trapper selected CDNAs to
prepare Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipellne with 384 multicapillary sequencer. Genome Res.
10 (11), 175-1771 (2000)
Computer-based methods for the mouse full-length CDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addebbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for /cell type="B6-derived CD11 +ve dendritic cells" /clone lib="RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells"

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source
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                                                                                                                                                                                   1519 CAATATAGACCATGTTTCTTCCAGACAAAGCCCATTAGGAA-CTTCAGCAGCAGTCACAC 1577
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 701)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Golobori,T., Baldarelli,R., Hill,D.P., Matsuda,H.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
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                                                                                           1459 TTAAAAATTCATGTTCACATTTTTCTGTCTCAGGACTGCATTTATTGCATGATATTCTGT
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    Length 705;
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                                                 Indels
       DB 6;
                                                   10;
    Score 665.6; DB 6;
Pred. No. 1.9e-150;
0; Mismatches 10;
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Query Match 26.4%;
Best Local Similarity 98.3%;
Matches 693; Conservative
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Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Porrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedaierski, R.M., King, B.L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lehard, B.L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pevan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Fillai, R., Pontius, J.U., Oi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Semple, C.A., Secou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wanger, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walls, C., Wang, Y., Watanabe, Y., Wang, L.G., Wilming, L.G., Wynshaw, Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yang, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wang, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wang, L.G., Whiming, L.G., Wynshaw, Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yang, L., Wahlestedt, C., Wang, Y., Carninci, P., Hayatsu, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subbraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--394-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000)

Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre Actababrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
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Adachi,J., Aizwa,K., Akimura,T., Arakawa,T., Carninci,P.,
Rukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kwai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M., and Hayashizaki,Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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/cell_type="NOD-derived CD11c +ve dendritic cells"

db_xref="taxon:10090" clone="F630012G18"

/organism="Mus mu /mol_type="mRNA" /strain="NOD"

us-10-812-620-1.rst

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/clone lib="RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 717)
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
                                                                                                                                                                              1029 GGATTCTCCTTTTCACATCTGTCTTGCACATCTGTCTTGCTCATGAGAATTGATATGAAG
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                                                                                                                                                                                                                                                                   GAAGAGGTAGAAAGCAGATGTCTGTATAAAGAGACTTTAATGGTCACTATGTCATCCTGT
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                                                                                         Score 655.2; DB 6;
Pred. No. 6.4e-148;
0; Mismatches 14;
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BY743963.1 GI:27170313
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Best Local Similarity 97.6%;
Matches 686; Conservative
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence-clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
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Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-2 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Rukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
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Takeda,Y., Waki,K., Watahiki,K., Watahiki,T., Tagami,M.,
Direct Submission
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Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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    van der Weyden,L.,
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., v Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., N Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                           Score 650.4; DB 9;
Pred. No. 9.3e-147;
0; Mismatches 7;
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/organism="Mus musculus"
/organisy="genomic DNA"
/db_xref="texon:10090"
/clone="MHPN371g15"
/clone_lib="MHPN"
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Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN371g15, genomic survey sequence.
CR071785.
CR071785.1 GI:49805375
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musina
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/clone="1830025C13"
/tissue_type="bone_marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched,
                                                                                                                                      Score 650.8; DB 6;
Pred. No. 7.5e-147;
0; Mismatches 9;
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                                                                                                                                  Musculus; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (2021) (Bases I to 674)

Rosana, I., Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N.; Saito, R., Suzuki, H., Yamanaka, I., Kuyadawa, H., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Mateuda, H., Batsel, K., W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Mardis, E.D., Kanagani, T., Kawasiwa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenle, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petovosky, M., Billak, R., Pontius, J.U., Oil, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, J.J., Setou, M., Shimada, K., Schneider, C., Remgle, C.A., Setou, M., Shimada, K., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Vang, I., Vang, I., Wallana, R., Taskenaka, Y., Taylor, M.S., Tasadale, R.D., Tomita, M., Vang, I., Wang, L., Vunan, Y., Zamer, A., Carninci, P., Haysteu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Itoh, M., Kagawa, I., Wala, A., Sato, K., Sato, Hara, A., Hashizume, W., Imotani, K., Indayawa, J., Vang, Rogers, J., Bilmey, E. and Hayashizaki, Y. Rasadi, D., Shibata, K., Shibata, R., Shinagawa, A., Yanayiso, E. the mouse transcriptome based on functional annotation of 60,770 full-length cDNa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 81-45-503-9216

Email: genome-reseges.riken.jp, URL:http://genome.ges.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Fukuda,S., Kanno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1677-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
                                                                                           musculus (house mouse)
                                 BY744630.1 GI:27171386
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and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                            /db_xrefe"taxon:10090"
/clone="1830042L06"
/tissue_type="bone marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                               ı,
                                                                                                                                                                                                                                                                                                                                                                                     Length 674;
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                                                                                                                                                                                                                                                                                                                                                                                 Score 643.2; DB 6;
Pred. No. 5.2e-145;
0; Mismatches 11;
                                                                                                                                                   organism="Mus musculus"
                                                                                   further details.
Location/Qualifiers
                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                     25.6%;
                                                                                                                                                                                                                                                                                                                      macrophage"
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.2
Matches 659; Conservative
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RESULT 11

BY747821

prepare mouse tissues. Tissues were provided by David A. Hume (Depts. of Biochemistry

Genetics Wellcome

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/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, NOD-derived CD11c
+ve dendritic cells"
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Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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                                                                              Figures were provided by Dr. John Todd (Dept. of Medical G
Wellcome Trust Centre for Molecular Mechanisms in Disease W
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp)
further details.
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Aukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,P.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Zano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
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BY747821 RIKEN full-length enriched, NOD-derived CD11c +ve
dendritic cells Mus musculus CDNA clone F630011J05 5', mRNA
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BY749084 RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus cDNA clone F630224E05 5', mRNA
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Direct Submission
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gracefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
| Strain="NOD" |
| Ab xref="texon:10090" |
| Colone="F630224E05" |
| Coll_type="NOD-derived CD11c +ve dendritic cells" |
| Clone lib="RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells" |
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Pred. No. 3.7e-143;
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/clone is among a rearrayed set of 15.47 Clones from 11 enbryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and R12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extrembryonic tissue of 7:5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978:"
43053D08-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3053D08 5', mRNA sequence.
BG080418
BG080418.2 GI:40014148
                                                                                                                                                                                                                                                                                                                                                                                                                     On Jan 26, 2001 this sequence version replaced gi:12562986.
Other ESTS: H3053D08-3
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Gassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@1gsun.grc.nia.nih.gov/cDNA/15k.html for details.
Visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3053 row: D column: 08
Seg primer: -21M13 Reverse
High quality sequence stop: 644
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 644)
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Tranka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X.,
Grahovac, M.J., Pantano, S., Sano, Y., Plao, Y., Nagaraja, R., Doi, H.,
Wood, W.H. III, Becker, K.G. and Ko, M.S. H.
Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental CDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
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Best Local Similarity 99.4%; Pred. No. 2.3e-141;
Matches 641; Conservative 0; Mismatches 3;
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db_xref="taxon:10090"
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Musualia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Musualia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (bases 1 to 645)

E. I (bases 1 to 645)

S. Yeruno, W., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Mareuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chorbani, L.E., Cousins, S., Dallak, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Guogh, J., Grimmond, S., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltis, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontus, J.U., Qi, D., Ramachandran, Ravasi, T., Reed, J.C., Reed, J.C., Reid, J., Ring, B.Z., Ringwald, M.,
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musculus cDNA clone 1830011F16 5', mRNA sequence.
GAACTITITAAAAAGAGGCCAAGGATICACCATICAAGACTCACTITCCAGGGGCTCTIT
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Indels

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Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wallestedt, C., Wang, Y., Watanabe, Y., Walle, C., Wilming, L.G., Wynahaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yang, T., Yang, T., Komner, A., Carninci, P., Hayatsune, N., Hirozane-Kishikawa, T., Komner, A., Carninci, P., Rakazune, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Sakazune, N., Kawai, J., Aizawa, K., Itoh, M., Xasunishi, A., Yashino, M., Waterston, K., Iander, E.S., Shinagawa, I., Watalyais, Y., Yashino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome, 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center, and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Adachi,J., Hashizume,M., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
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Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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/clone_lib="RIKEN full-length enriched, bone marrow
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Pred. No. 1.1e-140;
0; Mismatches 7; Indels 0
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1830011F16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
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"I (Dases 1 to 643)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kyoawa,H., Yaqi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
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Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond, S.,
Kawaii,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
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Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
61
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musculla cDNA clone I830018A02 5', mRNA sequence.
                                                               362 GTCCTTTGAACTGGAAACATTATCAATCTAGTTGTTATTTTTTCTCTACGACAACCTTGA
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2 GGTCTGTTAGTCTTGAACTTTTAAAAGAGGGCCAAGGATTCACCATTCAAGACTCACTT
                                                                                                                                                     182 CCCAAGTGCTCTCCTGGACGATAGCCGGGGCCTCCATCCTGTTTCTCAGTGGCTGTTTCA
                                                                                                                                                                                                                                             CCCAAGTGCTCTCTGGACGATAGCCGGGGCCTCCATCCTGTTTCTCAGTGGCTGTTTCA
                                                                                                                                                                                                                                                                                                      242 TCACCAGATGTGTCGTAACATATCGCAGCTCTCAAATTTCCGGGCAGAACTTACAGCCAC
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                                        62 TCCAGGGGCTCTTTCTAAACTGAGAAGGAAAGGAAAAGGAAGAAAGGCAGGAAAAAGGAA
                                                                                                                            AGTCCCTGAGCTTCTGGGATGCTGGGGAGCCCAACA 637
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629; Conservative

Matches

Similarity

2 GGTCTGTTACTCTTGAACTTTTAAAAGAGGCCAAGGATTCACCATTCAAGACTCACTT

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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-922
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1677-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Genome Encyclopedia Project of Genome Exploration Research Genome Encyclopedia Project of Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yana, Z., Y., Zimmer, A., Carninol, P., Savolan, M., Zhu, Y., Zimmer, A., Carninol, P., Sakazume, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imctani, K., Ishii, Y., Shinagawa, A., Yasunishi, A., Yoshino, W., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, W., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60, 770 full-length colbs.
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/clone_lib="RIKEN full-length enriched, bone marrow
macrophage"
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/clone="1830018A02"
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June 9, 2005, 13:17:52; Search time 185 Seconds (without alignments) 1892.774 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                            - nucleic search, using frame_plus_p2n model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	. :	376,	376,	376,	376,	376,	376,	376,	376,	376,	3, A	51,	20,
-	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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US-09-111-470-1	US-09-862-802A-1	ö	-09-111	39-86	-575-2	9-389	9-620	9-339	US-09-433-826B-29	US-09-604-287A-29	US-09-285-480-29	US-09-834-759-29	US-09-590-751A-29	US-09-551-621-29	0-2	US-09-016-434-698	9-591-435-1	US-09-591-435-9	US-09-517-605-1	US-09-591-435-11	9-949-016-4	US-08-365-103B-3	US-08-365-103B-5	US-08-365-103B-1	-09-111-	39-862-802A	09-111	-09-862-802A-	-09-949-016-40	-09-016-434-118	-09-535-521-1	US-09-535-521-12
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ALIGNMENTS

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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
Sequence 376, Application US/09907794A Patent No. 6635468
GENERAL INFORMATION: APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                               Godowski, Paul J.
Grimaldi, Christopher J.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Paoni, Nicholas F.
Roy, Margaret Ann
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Mather, Jennie P.
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Eaton, Dan L.
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Gao, Wei-Qiang
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### APPLICATION NUMBER: DCT/US99/2154

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14

CURRENT PILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 2001-07-22

PRIOR PILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

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PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/2164
                                                                                                                                                                                                             GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
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                        ThrGlnGluGluGluPheLeuPheArgThrLysProLysArgLysGluPheTyrlle
                                                                                                                                            GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr
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; Sequence 376, Application US/09905125A
; Patent No. 6664376
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
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Filvaroff, Ellen
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Gao, Wei-Qiang
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle
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Matches:
Conservative:
Mismatches:
Indels:
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            PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLILING DATE: 1999-07-28
PRIOR PLILING DATE: 1999-07-28
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-09
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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Scwart, Timothy A.
APPLICANT: Thouse, Daniel
APPLICANT: Thouse, Daniel
APPLICANT: Thing Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR FILING DATE: 1999-11-29
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PRIOR PLING DATE: 1999-12-02
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PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
                                                                                                                                                            Sequence 376, Application US/09902775A Patent No. 6686451
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Grimaldi, Christopher
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dan L.
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gao, Wei-Qiang
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|163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATC 222
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PRIOR FILING DATE: 1999-10-05
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PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PELICATION NUMBER: PCT/US99/28565
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PRIOR PLILNG DATE: 2000-01-05
NUMBER: PCT/US00/00219
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Grimaldi, Christopher J
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Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
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                                    Gerber, Hanspeter
Gerritsen, Mary E.
              Fong, Sherman
Sao, Wei-Qiang
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ORGANISM: Homo Sapien
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US-09-906-700-376
; Sequence 376, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Botstein, Avi
; APPLICANT: Botstein, David
; APPLICANT: Besnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
                                                                                                                7.27e-88
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PRIOR FILING DATE: 2000-01-05
          NUMBER OF SEQ ID NOS: 423
SEQ ID NO 376
LENGTH: 997
                                                 ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-775A-376
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APPLICANT: SCHEERE, TIMOCHY A.
APPLICANT: SCHEERE, TIMOCHY A.
APPLICANT: Mood, Williams, P. Mikkey
APPLICANT: Wood, Williams, P. Mikkey
APPLICANT: Williams, P. Mikkey
APPLICANT: Williams, P. Mikkey
TITLE OF INVENTION: Scheeted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPRENCE: 10066-18
CURRENT APPLICATION NUMBER: 105/09/906, 700
CURRENT FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-09-07-07
PRIOR FILING DATE: 1999-09-07-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/2054
PRIOR FILING DATE: 1999-09-13
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APPLICANT: Vindams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT APPLICATION NUMBER: POT/011
PRIOR APPLICATION NUMBER: POT/013048
PRIOR PILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 60/14,698
PRIOR APPLICATION NUMBER: US 60/14,698
PRIOR APPLICATION NUMBER: POT/01899/20594
PRIOR PILING DATE: 1999-07-28
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PRIOR PILING DATE: 1999-10-13
PRIOR PILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/2005
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PRIOR APPLICATION NUMBER: PCT/US99/2005
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                                      MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer
                                                                                                                           GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle
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Fatent No. 6767995
GEBERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Betsein, David
APPLICANT: Betsein, David
APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Goddard, A.
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                                                                                 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
                                                                                                                                     120 ThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
                                                                                                                                                      CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
                                          200 SerMetProTrpileCysGluMetProGluileSerProLeuAsp 214
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-26
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Godowski, Paul J.
Grimaldi, Christopher
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Forsara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wel-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J
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Paoni, Nicholas F.
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20948
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-12-02
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SEQ ID NO 376
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CORGANISM: Homo Sapien
US-09-904-920A-376
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US-09-905-381A-376
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APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILER ENERSENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
PRIOR PLILING DATE: 2000-02-22
PRIOR PLILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-07-26
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PRIOR PLILING DATE: 1999-07-28
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PRIOR PLILING DATE: 1999-09-08-08
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                                                                                                                        GGACTGTCAGACCAGGTTGTCGAGGGTCAGTGGCAATGGGTGGACGGCACACCTTTGACA 582
                               GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys
                                                      200 SerMetProTrpileCysGluMetProGluileSerProLeuAsp 214
                                                                                                                                                                                                           703 AATTATTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTGAAC 747
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Patent No. 6818449
GENERAL INFORMATION:
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Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Rahavin, Ivar J.
Pan, James
Paoni, Nicholas F.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dan L.
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223 ACCAGATGTGTGTGACATTTCGCATCTTTCAAACCTGTGATGAGAAAAGTTTCAGCTA
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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               PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2090-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 376
LENGTH: 997
  PCT/US99/28565
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APPLICATION NUMBER: PCT FILING DATE: 1999-12-02
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APPLICANT: ROY, MARGARE F.
APPLICANT: SCARATE, Timchy A.
APPLICANT: Stewart, Timchy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT FILING DATE: 10466-14
FRIOR FILING DATE: 1040-07-13
FRIOR FILING DATE: 1040-07-2
FRIOR PELICANTON NUMBER: PCT/US99/2054
FRIOR FILING DATE: 1039-0-0-16
FRIOR FILING DATE: 1039-0-0-16
FRIOR PELICANTON NUMBER: PCT/US99/2014
FRIOR APPLICATION NUMBER: PCT/US99/2014
FRIOR APPLICATION NUMBER: PCT/US99/2016
FRIOR APPLICATION NUMBER: PCT/US99/2019
FRIOR APPLICATION NUMBER: PCT/US99/2019
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FRIOR FILING DATE: 1999-12-20
FRIOR APPLICATION NUMBER: PCT/US99/2019
FRIOR FILING DATE: 1999-12-20
FRIOR APPLICATION NUMBER: PCT/US99/2019
FRIOR FILING DATE: 1999-12-20
F
Sequence 376, Application US/09905381A Patent No. 6818746 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                              APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                          Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
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; ORGANISM: Homo Sapien
US-09-905-381A-376
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283 CCTGAGAATTTCACAGAGCTCTCCTGCTACAATTATGGATCAGGTTCAGTCAAGAATTGT 342
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Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                  US-10-812-620-2 (1-214) x US-09-905-381A-376 (1-997)
                                                                                    Indels:
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Patent No. 6828146
GENERAL INFORMATION:
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
7.27e-88
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79.07%
66.51%
65.65%
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Goddard, A.
Godowski, Paul J.
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Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                          Percent Similarity:
Best Local Similarity:
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UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro
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COMPUTER: IDAD PO disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURENTLY HEREMITH
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKET DAVIG L.
REGISCHATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTXD:493
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 512/418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-772-440-3; Sequence 3, Application US/08772440; Patent No. 6046158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ariizumi, Kiyoshi
APPLICANT: Takashima, Akira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: UNITITLE OF INVENTION: LECTITLE OF INVENTION: THE NUMBER OF SEQUENCES: 42 CORRESCONDENCE ADDRESS: ADDRESSEE: ADDRESSEE: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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APPLICANT: Thumas, Daniel
APPLICANT: Thumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
GURRENT APPLICATION NUMBER: US/09/906,618
GURRENT FILING DATE: 2001-07-16
FRIOR FILING DATE: 1090-07-07
FRIOR PELICATION NUMBER: US 60/145,698
FRIOR PELICATION NUMBER: US 60/146,222
FRIOR FILING DATE: 1999-07-07
FRIOR APPLICATION NUMBER: PCT/US99/2094
FRIOR FILING DATE: 1999-09-13
FRIOR APPLICATION NUMBER: PCT/US99/21090
FRIOR APPLICATION NUMBER: PCT/US99/21090
FRIOR APPLICATION NUMBER: PCT/US99/21090
FRIOR APPLICATION NUMBER: PCT/US99/21090
FRIOR PELING DATE: 1999-09-15
FRIOR PELING DATE: 1999-09-15
FRIOR PELING DATE: 1999-11-30
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                           Timothy A.
                                                                                                                Pan, James
Paoni, Nicholas F.
                                                                                                                                                         Roy, Margaret Ann
Stewart, Timothy
                                                                    Kljavin, Ivar J.
Mather, Jennie P.
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Best Local Similarity:
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APPLICANT:
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Conservative:
Mismatches:
Indels:
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Patent No. 6476195
GENERAL INFORMATION:
APPLICANT: ROSen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER FILING DATE: 1999-07-29
EARLIER FILING DATE: 1999-07-20
EARLIER FILING DATE: 1998-07-30
EARLIER FILING DATE: 1998-07-30
EARLIER FILING DATE: 1998-07-30
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                                                                                                                         Length:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1227 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                   1.99e-39
392.50
59.16%
41.88%
                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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585 ACT--CTCAGGGAGAAAACTGTGTTGTTCTT---GTTTATAACCAAGATAAATGGGCCT 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 AAGTTÄGAGCACCÄTGCAAAGCTCAAATGCÄTCAAAGÄGAAATCÄGAACTGAAAAGTGCT
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Patent No. 6046158
GENERAL INFORMATION:
APPLICANT: Arizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
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Matches:
Conservative:
Mismatches:
Indels:
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EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-12
EARLIER FILING DATE: 1998-08-12
EARLIER PRING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
SARUIER FILING DATE: 1998-08-06
SOFTWARE: PARCHIN VOICE: 1998-08-06
SOFTWARE: PARCHIN VOICE: 1998-08-06
SOFTWARE: PARCHIN VOICE: 2.0
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359.00
58.59%
39.39%
                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-489-847-51
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                        LENGTH: 2076
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102 AICAACAGGCTCTTCTGCAGGTTCCAAGGAGAGGACTGCCCCTCTCAAAAGTAATACC 361
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Saciand, Odile
APPLICANT: Bates, Elizabeth E.M.
APPLICANT: Saciand, Sem
APPLICANT: Saciand, Sem
APPLICANT: Construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construc
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COMPUTER: IBM PC Compatible
OPERATES: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 60/053,080
FILING DATE: 09-UUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: SF0695
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: DNAX Research Institute
901 California Avenue
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APPLICATION NUMBER: US/09/111,470
FILING DATE: 08-JUL-1998
                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/09111470
; Patent No. 6277959
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
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STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                  208 ProGluile 210
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487 AAGAAGATT 495
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STATE: California
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ZIP: 94304-1104
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COCATION:
US-09-111-470-1
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Pred. No.:
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LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES THEREOF
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                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pather, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 12,165
REFERENCE/DOCKET NUMBER: 12,105
REFERENCE/SOCKET NUMBER: 23,065
TELEPHONE: 512/414-7577
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
TENGTH: 501 base pairs
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Mismatches:
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Matches:
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                                                           NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
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58.90%
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TYPE: nucleic acid
STRANDEDNESS: single
TITLE OF INVENTION:
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Best Local Similarity:
                                                                                                                                                                                    CITY: Houston
STATE: Texas
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122 TICTTTATIGCTTTIGECATTTTCTTTCAAAAATATTTCTCAGCTTCTIGAAAAAAAGACT 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          722 TCTGCTTATTTTGTGGGGCTCTCAGAAGGTCAGAAGGTCAGCGACATTGGCAATGGGTTGAT 781
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                                                                                                                                                                                                                                                                                GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeu---
                    1104
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Matches:
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Patent No. 6476195
GENERAL INFORMATION:
GENERAL INFORMATION:
JENERAL INFORMATION:
APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: P2031P1
CURRENT APPLICATION NUMBER: US/09/489, 847
CURRENT FILING DATE: 2000-01-24
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER PILING DATE: 1998-08-12
EARLIER FILING DATE: 1998-08-12
EARLIER FILING DATE: 1998-08-12
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EARLIER FILING DATE: 1998-08-12
EARLIER FILING DATE: 1998-08-12
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Best Local Similarity:
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  Alignment Scores
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## Sequence 1, Application US/09862802A

## APPLICANT: Ravel, Odile

## APPLICANT: Ravel, Odile

## APPLICANT: Bates, Elizabeth Ester Mary

## APPLICANT: Bates, Elizabeth Ester Mary

## APPLICANT: Lebecque, Serge J.E.

## APPLICANT: Lebecque, Serge J.E.

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## APPLICANT: Lebecque, Serge J.E.

## APPLICANT: Lebecque, Serge J.E.

## APPLICANT: Lebecque, Serge J.E.

## CURRENT APPLICATION NUMBER: US 60/053,080

## PRIOR FILING DATE: 1998-07-09

## PRIOR FILING DATE: 1998-07-08

## NUMBER OF SEQ ID NOS: 13

## SEQ ID NO: 13

## ERWARE: PatentIn version 3.1

## ERWARE: PatentIn version 3.1

## ERWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                          SerValLysAsnCysCysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePhe 94
  --SerGly 37
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| NAME/KEY: CDS
| LOCATION: (242)...(952)
| OTHER INFORMATION:
| US-09-862-802A-1
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Matches:
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EARLIER FILING DATE: 1998-08-06
BARLIER APPLICATION WUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 119
LENGTH: 2059
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39.60%
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ORGANISM: Homo sapiens
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Mammatis bunieria; Kodentia; Scilloghann; Muridae; Murinae; Mus. B. 1 (Dases 1 to 1666)

Strausberg.R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg.B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheefz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheefz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Abramson, R.D., Mullahy, S.J., Bossak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Garcia, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, R.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
             BC000715 Homo sapi
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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MUS musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9, mRNA (cDNA clone MGC:5682 IMAGE:3158063), complete cds.
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                                               Command line parameters:
-MODEL=frame+ pan.model -DBV=xlh
-Q=/Cgn2_1/USPTO_gepool/VS1081260/runat_07062005_124336_3244/app_query.fasta_1.391
-Q=/Cgn2_1/USPTO_gepool/VS10812620/runat_07062005_124336_3244/app_query.fasta_1.391
-Q=/Cgn2_1/USPTO_gepool/VS108128-pon.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=DOONUGOOOO
-UNITS=bits -NORM=ext -HEAPSIZE=560 -MINLEN=0 -MAXLEN=200000000
-USFR=US10812620_@CGN 1 1_4200_@runat_07062005_124336_3244 -NCPU=6 -ICPU=3
-NORMAP-LARGEQUERSY -NEG SCORES=0 -MATR -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPORT=0.5 -FGAPOP=6
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                           OM protein - nucleic search, using frame_plus_p2n model
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9910161.
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SLSFWDAGEPNNIVLVEDCATIRDSSNSRKNWDIPCFYSPWNICEGMPENSPLD"
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ξ
                                                                                                                                                                                      Submitted (20-PEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunazarne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
TobNa Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Contact: MGC help desk
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DB:
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AB024717 2517 bp mRNA linear ROD 10-NOV-1999
Mus musculus mRNA for macrophage C-type lectin Mincle, complete
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                                   142 CAAGTGCTCTCCTGGACGATAGCCGGGGCCTCCATCTTGTTTTCTCAGTGGCTGTTTTCATC 201
                                                                                                                                                                                                                                                                                                                                                                         262 AGAAATATTAAGGAGCTTTCCTGCTACAGTGAGGCATCAGGTTCAGTCAAGAATTGCTGT 321
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Mincle; macrophage C-type lectin Mincle.
Mus musculus (house mouse)
Mus musculus
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J. Immunol. 163 (9), 5039-5048 (1999)
99458965
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Akira, S. and Matsumoto, M.
Direct Submission
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bulkaryota, Eutheria; Rodentia, Sciurognathi; Muridae, Murinae, Mus.
Bi (lases 1 to 2517)
Sinta,S. and Matsumoto,M.
Novel C lectin and gene thereof
L Patent: JP 2001112482-A 1 24-APR-2001;
SCIENCE & TECH AGENCY
OS Mus sp. (mouse)
PN JP 2001112482-A/1
PD 24-APR-2001
PP 15-OCT-1999 JP 1999293724
PI SHIZUO SHINRA, MAKOTO MATSUMOTO
PC C1201/69, A61K38/00, A61P31/00, A61P37/04, A61P43/00, CO7K14/47,
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Query Match:
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SLSFWDAGEPNNIVLVEDCATIRDSSNSRKNWNDIPCFYSWPWICEMPEISFLD"
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Fax:81-6-6879-8305)
Location/Qualifiers
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Conservative:
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Gaps:
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Rattus norvegicus macrophage-inducible C-type lectin (Clecsf9)
mRNA, complete cds.

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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                              544 crdacadaccadgrdcrddadddaddaddaddadacaccrrrcacadad
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                               ProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeuThr
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1 (bases 1 to 730)

Flormes,L.M., Bryceson,Y.T., Spurkland,A., Lorentzen,J.C.,
Dissen,E. and Fossum,S.
Identification of Lectin-like receptors expressed by antigen
presenting cells and neutrophils and their mapping to a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10116"
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receptor gene complex; APLEC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cumunogenetics 56 (7), 506-517 (2004)

2 (bases 1 to 730)

3 Florenes,L.W., Dissen,E. and Fossum,S.

Direct Submission

Submitted (06-AUG-2003) Anatomy, University of Oslo, PO Box Blindern, Oslo 0317, Norway

Blindern, Oslo 0317, Norway

1. 730

/mol types="Rattus norvegicus"

/mol types="Rattus norvegicus"

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51. .698
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eu (bases 1 to 2517)

Akira, S. and Matsumoco, M.

A novel C-type lectin and its genes

L Patent: WO 0127271-A 1 19-APR-2001;

JAPAN SCIENCE AND TECHNOLOGY CORP, SHIZUO AKIRA, MAKOTO MATSUMOTO
OS Mus sp. (mouse)

PN WO 0127271-A/1

PD 19-APR-2001

PR 02-OCT-2000 WO 2000JP006820

PR 15-OCT-1999 JP 99P 293724

PI SHIZUO AKIRA, MAKOTO MATSUMOTO
PC C12N15/12, CO7K14/47, C12Q1/68, A61K38/17, A61P31/00, A61P37/04, PC
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              SerLeuSerPheTrpAspAlaGlyGluBroAsnAsnIleValLeuValGluAspCysAla
                                                                         GlnValLeuSerTrpThr11eAlaGlyAlaSer11eLeuPheLeuSerGlyCysPheIle
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LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu
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BD094039.1 GI:22639627
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Riausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheafer, C.F., Bhat, N.K.,
Hopking, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Hafeh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownsteah, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, W., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Blockson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerztield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Schein, J.E., Jones, S.J. and Marza, M.A.,
Generation and initial analysis of more than 15,000 full-length
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/product="C-type lectin, superfamily member 9"
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SLSFWDVGEPNNIATLEDCATMRDSSNPRQNWNDVTCFLNYFRICEMVGINPLNKGKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 7 Row: i Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (15-NO-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-romail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:12653848.
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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//sh mer="nunom=p="
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/clone="MGC:1246 IMAGE:3507103"
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                             AUTHORS
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ESLSFWDAGEPNNIVFVEDCATWRDSSNPRKOWNDVSCFFSMPAICEMPBISPLD"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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| CATAAAACTATTAAGGAGCTTTCCTGCTACCTTGAAGCATCAGGTTCAGTCAAGAATTGC
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Homo sapiens
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Secreted and transmembrane polypeptides and nucleic acids encoding the same.
BD17243.
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JP 2002223786-A/316.
Homo sapiens (human)
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TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC 518
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Matches:
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                                                       /note="Incyte ID No: 1521513CB1"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Memo sapiens
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                        Lal,P., Yue,H., Tang,Y.T., Bandman,O., Burford,N., Azimzal,Y., Baughn,M.R., Lu,D.A. and Patterson,C.
Membrane associated proteins
Patent: WO 0112662-A 40 22-FBB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerMetProTrplleCysGluMetProGlulleSerProLeuAsp 214
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/ Organism="Homo sapiens"
/mol_type="genomic DNA"
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8-DEC-2001 JP 2001385248
7-SEP-1997 US 60/05911
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|163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
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/organism='Homo sapiens (human)'.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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C (12P21/02//C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19), C (C12N5/10, C12R1:91), C12N15/00, C12N5/00, (C12N5/00, C12R1:91) CC Secreted and transmembrane polypeptides and nucleic C acids
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                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalla, Butherla, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 997) (bases Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JEAN YUAN
C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer
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60,063354
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60,064103
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Location/Qualiflers
1. .997
Location/Qualiflers
1. .997
Mol Lype="genomic DNa"
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60/059121,17-SEP-1997 US

60/059121,17-SEP-1997 US

60/05926,15-OCT-1997 US

60/062287,17-OCT-1997 US

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60/063120,24-OCT-1997 US

60/063120,24-OCT-1997 US

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60/063120,29-OCT-1997                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted and transmembrane polypeptides and
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Mismatches:
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GENENTECH INC
                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
JP 2002238588-A/316
27-AuG-2000
18-DEC-2001 JP 2001385315
17-SEP-1997 US 60/059115
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774.00
79.07%
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JP 2002238588-A/316.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          883 CCTGAGAATTTCACAGAGCTCTCCTGCTACAATTATGGATCAGGTTCAGTCAAGAATTGT 342
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TCCTGGGCGTTAAGTTTAAAGAACTGCTCACCATGGGGGCTCACCTGGTGGTTATCAAC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrGlnGluGluGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||:::
|163 CAAATGTTCTTATGGACTGTTGCTGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
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  encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 ACCAGATGTGTTGTGACATTTCGCATCTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetabnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
     acids
                                                                                                                 (human)
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                                                 Location/Qualifiers
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Location/Qualifiers
     transmembrane polypeptides and nucleic
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Matches:
Conservative:
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C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19), (C12N5/10,
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                                                                                                                                                                                                                                             JEAN YUAN
C12N15/09, A61K45/00, A61P1/00, A61P13/12, A61P17/00, A61P17/06,
                                                                                                                                                                                                                                                                                         A61P25/16, A61P25/28, A61P31/12, A61P35/00, C07K14/47, C07K16/18,
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/organism="Homo sapiens"
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JIAN ZHENG,
    Length:
Matches:
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Indels:
60/063045, 24-OCT-1997 UG
60/063329, 27-OCT-1997 UG
60/06354, 28-OCT-1997 UG
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60/066846, 18-NOV-1997 UG
60/066120, 21-NOV-1997 UG
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                            223 ACCAGATGTGTGAGATTTCGCATCTTTCAAACCTGTGATGAGAAAAGTTTCAGCTA 282
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 997)

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                                                                  ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro
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60/059117 PR
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60/059263 PR
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60/063127 PR
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GENENTECH INC
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JP 2002253280-A/316
10-SEP-2000
18-DEC-2001 JP 2001385319
17-SEP-1997 US 60/059115
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JP 2002253280-A/316.
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Ashkenazi, A., Botstein, D., Desnoyers, L., Eston, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kijavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
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TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC
                                                                                         120 ThrGlnGluGluGluGluPheLeuPheArgThrLysProLysArgLysGluPheTyrile
                                                                                                                                             140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPhsThr
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/mol_type="genomic DNA"
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Sequence 376 from patent
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Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N., Filvazoff, B., Fong, S., Gao, W.-Q., Gerber, H., Gerriteen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kijavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
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                                                                                                                 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
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|CAAATGTTCTTATGGACTGTTGGTGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATC 222
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                          GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr
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Desnoyese, L., Goddard, A., Godowski, P.J., Gurney, A.L., Mather, J.P., Williams, P.M. and Wood, W.I.
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Cy8ProLeuAsnTrpLy8HisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu
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TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTGTTATCAAC
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/mol_type="genomic DN
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Sequence 376 from patent
AR473298
AR473298.1 GI:42708673
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                                         79
          GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys
                                                     283 CCTGAGAATTTCACAGAGCTCTCCTGCTACAATTATGGATCAGGTTCAGGTTCAGAATTGT
ThrargCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro
                                      60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys
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Mincle, C-type lectin, antinflammatory, macrophage, inflammation, disorder, nuclear factor interleukin 6; NF-IL6; 88.
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/product= "Mincle"
/note= "C-type lectin"
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ACD13915
ACD09695
ACC88440
ACD21180
ABX75552
ADC78688

AAF72432

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-MODEL-frame+ p2n.model -DEV=xlh
-O-Capl2 1/USFTO 8p001/USI08126201
-O-Capl2 1/USFTO 8p001/USI0812620/runat 07062005 124335 3234/app_query.fasta_1.391
-O-Capl2 1/USFTO 8p001/USI0812620/runat 07062005 124335 3234/app_query.fasta_1.391
-DB=N Geneseq_16Dec04 -OFMT-fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=humman40.cdi
-LIST=45 -DOCALIGN=200 -TNR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=ptc -NOFMS=ext - HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=USI0813620 @CGN 1 1 644 @runat 07062005 124335 3234 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=10 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPERT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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Adf80738 Human hep
Adr41300 Human CD-
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                               nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                              17-AUG-1999;
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                                                                                    AAF81743;
                              RESULT 2
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                                                                                                                                                                This invention relates to a C-type lectin, termed Mincle, which is formed from a transcriptional target gene of nuclear factor interleukin 6 (NF-116). Mincle is a macrophage activating protein which can be used in the treatment of immune disorders, and inflammation. Compositions containing the protein have immunomodulatory and antiinflammatory activity. The present sequence represents murine cDNA encoding Mincle
                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 TrpSerSerSerLeuLyaAsnCysSerAspMetGlyAlaHisLeuValValIleAspThr 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 ACCAGATGTGTCGTAACATATCGCAGCTCTCAAATTTCCGGGCAGAACTTACAGCCACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        604 TCCCTGAGCTTCTGGGATGCTGGGGAGCCCAACAATATAGTTTTGGTGGAGGACTGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 IGGICATCAAGITTAAAGAATIGCTCAGACAIGGGGGCTCACCTGGTGGTATCGACACA
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                                                                                               New macrophage activating C-type lectin for the treatment of immune disorders and inflammation.
                                                                                                                                                                                                                                                                 Sequence 2517 BP; 756 A; 533 C; 463 G; 765 T; 0 U; 0 Other;
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(NISC-) JAPAN SCI & TECHNOLOGY CORP.
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AAF81741 to AAF81777 encode the human membrane associated proteins

(MEMAP) given in AAB74695 to AAB74731. MEWAPS have cytostatic,

continifiammatory, anticonvollabant, immunosuppressive, antidiarrheic and

antiarteriosclerotic activities, which can be used in gene therapy.

Continifiammatory, anticonvollabant, immunosuppressive, antidiarrheic and

antiarteriosclerotic activities, which can be used in gene therapy.

MEMAPS and agonist of MEWAPS can be used to treat a disease or condition

Confered with decreased expression of functional MEMAP. These disorders include cell

Conference are used to treat a disease or condition associated with

Conference are used to treat a disease or condition associated with

Conference and memaPy polynuclectides and proteins are also used for the

disponsis of these disorders. Specific examples of these disorders

Conference and memaPy polynuclectides and proteins are also used for the

Conference and memaPy polynuclectides and proteins and small

Conference memaPy polynuclectides can be used to prepare transagentc

Conference MEMAP polynuclectides can be used to prepare transagentc

almals which can be studied to provide information concerning human

disease. Anti-MEMAP antibodies are useful in immunoassays for the

Conference on MEMAP protein and can be used as antagonists to treat or

prevent a disorder associated with MEMAP. Polynuclectides encoding MEMAP

Con be delivered to target cells with genetic abnormalities with respect

Con the expression of MEMAP to treat or prevent a disorder associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide with a human membrane associated protein sequence is useful for the diagnosis, prevention and treatment of cell proliferative, autoimmune/inflammatory, neurological and gastrointestinal disorders.
                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic; antiarteriosoclerotic; gene therapy; call proliferative disorder; autoimmune disorder; inflammatory disorder; neurological disorder; gastrointestinal disorder; cancer; inflammation, atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                    diagnosis; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burford N, Azimzai Y;
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                                                                                                                                                                                                                                                         Human membrane associated protein MEMAP-3 encoding cDNA.
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ВР
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99US-0164203P.
AAF81743 standard; cDNA; 968
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R, Lu DAM, Pat
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Conservative:

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AlaThrileArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
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TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGGCTCACCTGGTGGTTATCAAC 518
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| CAAATGTTCTTATGGACTGTTGCTGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATC 278
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                                                                           GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
                                                                                                         ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
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                                                                                                                                                                      CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
                                            HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       marker; chronic hepatitis; liver cirrhosis;
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AATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTGAAC
2 2 43
Mismatches:
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66.518
65.658
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hepatic carcinoma; human;
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Similarity:
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The present invention relates to hepatic-fibrosis disease markers (APP9032-APP9031). The APP9032-APP9031). The Sequences are useful for detecting and treating hepatic fibrosis caused by alcohol consumption, virus infection, etc., and the associated chronic hepatitis, etc. leading to liver firshosis and hepatic carcinoma. The markers allow the cause of hepatic fibrosis to be clarified (diagnostic precision), so more suitable treatments can be developed and given.
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                                                                          Hepatic fibrosis disease markers comprising polynucleotides or antibodies, useful for improved diagnosis, screening and developing drugs to treat hepatitis, to control cirrhosis and carcinoms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218
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TCCTGGGCGTTAAGTTTAAAGAACTGCTCACCATGGGGGCTCACCTGGTGGTTATCAAC
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Matches:
Conservative:
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                                                                                                                                                          Claim 1; SEQ ID NO 200; 313pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; Als; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair; sg.
                                                                                                                                         СуяРгоцецАвлТтрLувНівТугGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
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                                                                      HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys
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97US-0059115P.
97US-0059117P.
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97US-0059266P.
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17-OCT-1997;
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prevention; immune disorder; immunodeficiency; autoimmune disorder;

prevention; immune disorder; immunodeficiency; autoimmune disorder;

thrombolytic disorder; hyperpoliferative disorder; cancer; tumour;

w proptotic disorder; neovascular disorder; respiratory disorder;

angiogenic disorder; neovascularisation, neurological disorder;

angiogenic disorder; reproductive system disorder; infectious disease;

chadocrine disorder; reproductive system disorder; infectious disease;

chadocrine disorder; reproductive system disorder; infectious disease;

chadocrine mapping; forensic analysis; immunophenotyping; cytostatic;

chadocric tranquiliser; vulnerary; antiinflammatory; nephrotropic;

cardiant; antiallergic, anti-HIV; antirheumatic; antiarthic;

antipsoriatic; immunosuppressive; vasotropic; nootropic; neuroprotective;

m antibsocterial; dermatological; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides and polypeptides useful for treating, preventing or ameliorating cardiovascular, renal, neurovascular, and autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to 167 novel human CD (cluster of differentiation) like molecules (ADR41388-ADR41563) and to cDNAs encoding them (seqid:11}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 342 A; 192 C; 206 G; 249 T; 0 U; 1 Other;
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Matches:
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                                                      ADR41300 standard; cDNA; 990 BP
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                                                                                        ADR41300;
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Claim 2; Fig 121; 320pp; English.
970S-0063287P.
970S-0063486P.
970S-0063816P.
970S-0063120P.
970S-0063120P.
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970S-0063329P.
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97US-0066466P.
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97US-0066770P.
97US-0066772P.
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P-PSDB; AAY13403.
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24-0CT-1997;
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Human PRO244 CDNA
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                                                                                                                                                                                                                                                                                                                                                                                  AAX52213-74 encode secreted and transmembrane human proteins, and are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have pecific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithalial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parcises. Alzheimer's disease, ALS, neuropathies or cancer. Pro255 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract
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                                                                                                                                                                                                                      New isolated human genes and polypeptides used in, e.g. treatment gastrointestinal ulceration.
                                                              Goddard A, Pennica D, Chen J, Yuan J;
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TCCTGGGCGTTAAAGTAGAACTGCTCAGCCATGGGGGGCTCACCTGGTGGTTATCAAC
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GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
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TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC
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ME, Goddard A
Kljavin IJ;
Tumas D;
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I, Gerritsen M
Hillan KJ, K
Stewart TA,
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99WO-US028565.
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99US-0145698P.
99US-0146222P.
99WO-US020594.
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99WO-US021547.
99WO-US023089.
99WO-US028214.
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15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel nucleic acid encoding a PRO polypeptide. The polypeptides and polynucleotides of the invention may be useful as research tools and as therapeutics for treating enterocolitis, Zollinger-Blison syndrome, gastrointestinal ulceration, psoriasis, cancer, Parkinson's disease, Alzheimer's disease, AlS, neuropathies, dermal scarting and wound healing, nerve repair, thrombosis, bone and/or cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple sclerosis, inflammatory disorders, atherosclerosis, cardiac injury, infertility, premature aging, AliS, diabetes compilications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.
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nerve repair; thrombosis; bone; cartilage formation; angiogenesis; asthmatory disorder; atheroacoid arthritis; multiple sclerosis; inflammatory disorder; atherosclerosis; cardiac injury; infertility; premature aging; AIDS; diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.
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Best Local Similarity:
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P-PSDB; ADC78689.
                                                                                                                                                                       WO200015796-A2
                                                                                                                            Homo sapiens.
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Yuan J;
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18-APR-2000;
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21-MAR-2000;
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11-APR-2000;
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11-APR-2000;
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                                                                                                                                              The present sequence is one of sixty one nucleic acids encoding novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. lung stranson's disease), wound repair, cardiovascular disorders (e.g. Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222
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TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGGCTCACCTGGTGGTTATCAAC 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  accagargricirgicacarrrcgcarcrrrcaaaccrgrgargagaaaagrrrcagcra 282
                                             Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
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| CAAATGTTCTTATGGACTGTTGCTGGGATCCCCCATCCTATTTCTCAGTGCCTGTTTCATC
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Conservative:
Mismatches:
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                                                                                                                      Claim 2; Fig 121; 393pp; English.
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774.00
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2001-081051/09
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Best Local Similarity:
               P-PSDB; AAB80271
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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder; PCR primer.
GCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGAATGATGTAACCTGTTTCCTC 702
                                                 200 SerMetProTrplleCysGluMetProGluIleSerProLeuAsp
                                                                          :::
AATTATTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTGAAC
                                                                                                                                                                                                                                                                                                                                                    Human DNA encoding PRO polypeptide seguence #12
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2000US-0195975P
2000US-0196107P
2000US-0196107P
2000US-019680P
2000US-0196820P
2000US-019858EP
2000US-019858EP
2000US-019959FP
2000US-0199550P
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2000WO-US023328
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                                                                                                                                                                                                         Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a comparing the level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human contacted with it. A specific polypeptide can be used to stimulate the proliferation of differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also can susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian choses, prostate, rectal, cervical, or liver tumours, in mammalian constitution be used for genetic analysis of individuals with genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 ccrgagaarrrcacagagcrcrccrgcracaarranggarcaggrcagrcaagaarrgr 342
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                                                                                                           Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and screen for modulators of the compounds.
          Gurney AL;
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Goddard A, Godo
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                                                                                                                                                                              Claim 2; Fig 23; 774pp; English.
       P, Chen J, Desnoyers L
Smith V, Watanabe CK,
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                                                        WPI; 2001-602746/68
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Best Local Similarity:
                                                                            P-PSDB; AAU29035
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                                     AlaThrileArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
                                               GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys
                                                                                                                                                                                                       Human; ss; gene; secreted protein; transmembrane protein; PRO; gene therapy; chromosome identification; chromosome marker.
                                                                                    SerMetProTrpileCysGluMetProGluIleSerProLeuAsp 214
                                                                                                                                                                                     Human cDNA for secreted/transmembrane protein PRO244.
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                                                                                                              RESULT
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The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of a secreted/transmembrane polypeptides, or PRO polypeptides or encoding a PRO protein extracellular domain. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, producing a PRO polypeptide (by culturing the host cell for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture), an isolated PRO polypeptide (having at least 80% sequence identity to: (a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino acid sequence selected from the 61 PRO proteins; (b) an amino acid sequence selected from the 61 PRO proteins; (c) an amino acid sequence selected from the 61 PRO potential domain of a PRO polypeptide or to a PRO polypeptide lacking its associated signal compisated, a chimmeeric modecule comprising a PRO polypeptide or to a PRO polypeptide lacking its associated signal compisation and acid sequence, an anti-PRO antibody, detecting a hoactive molecule to a cell expressing a PRO245 or PRO1868 and linking a bloactive molecule to a cell expressing a PRO PRO1868 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrara N;
n ME, Goddard A;
Kljavin IJ;
, TumaB D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, in generating probes and in tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney AL, Hillan KJ,
F, Roy MA, Stewart TA,
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W, Gerber H, Gerritse
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Filvaroff E, Fong S, Gao W, (
Godowski PJ, Crimaldi JC, Gurn
Mather JP, Pan J, Paoni NF, I
Williams PM, Wood WI,
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99WO-US030999.
2000WO-US00219.
2000WO-US00365.
2000WO-US004414.
97US-0065846P.
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modulating at least one biological activity of a cell expressing a PRO245 or PRO1868. Nucleic acids which encode PRO can be used to generate either transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence encodes a PRO protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342
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| CAAATGTTCTTATGGACTGTTGCTGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATC 222
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AATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTGAAC
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 Human; PRO polypeptide; secreted protein; transmembrane protein; chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical; liver; cancer; TRI-alpha; runour necrosis factor-alpha; proliferation; differentiation; chondrocyte cell; bone disorder; cartilage disorder; sports injury; arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;
                               cDNA encoding human PRO polypeptide #12.
                                                                                                                                                                        970S-0059263P.
970S-0059266P.
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11-MAR-1998
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20-MAR-1998
27-MAR-1998
31-MAR-1998
31-MAR-1998
31-MAR-1998
01-APR-1998
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17-DEC-1997;
18-DEC-1997;
              09-JUL-2003
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ACA89386;
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ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
                                                                                                                                                                                                                      ThrGlnGluGluGluDheLeuPheArgThrLy@ProLy@ArgLy@GluPheTyrlle 139
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                                                                                                                                                                            TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC 462
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    223 ACCAGATGTGTTGTGACATTTCGCATCTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTA 282
                                                                342
                                                                                            CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
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                                                                                                                                                                                                                                                                                    GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr
                                                                                                                                                                                                                                                                                                                                                 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys
                              60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys
                                                                                                                                                                                                                                                                                                     TCACAGGAGGAGCAGGAATTCCTTTCCTACAAGAACCTAAAATGAGAGAGTTTTTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted/transmembrane protein (PRO) cDNA #12.
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98WO-US019330.
98WO-US021141.
98US-00187368.
98US-002054311.
99WO-US025108.
99WO-US05028.
99WO-US010733.
99WO-US010733.
99WO-US010733.
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07-DEC-1998;
08-MAR-1999;
08-MAR-1999;
14-MAY-1999;
14-MAY-1999;
25-AUG-1999;
25-AUG-1999;
25-AUG-1999;
25-AUG-1999;
01-SEP-1999;
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202
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Matches:
Conservative:
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98US-0096891P

98US-0096947P

98US-0096949P

98US-0096959P

98US-0097022P

98US-0097022P

98US-0097974P

98US-0097974P

98US-0098014P

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98US-0102684P.
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774.00
79.07$
66.51$
65.65$
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Best Local Similarity:
17-AUG-1998;
17-AUG-1998;
18-AUG-1998;
18-AUG-1998;
26-AUG-1998;
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24-SEP-1998,
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30-SEP-1998;
30-SEP-1998;
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The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane), sequences 80% identical to them, or encoding a PRO polypeptide lacking its associated signal peptide or an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide. Also included are the encoded PRO proteins, PRO expression vectors, host cells transformed with the vector (used to produce PRO proteins), a chimaeric molecule comprising the PRO polypeptide fused to a chimaeric molecule comprising the PRO antibody, a method for stimulating the release of tunor necrosis factor alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Three hundred and five nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, and for detecting the presence of tumor in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ', Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL; Smith V, Watanabe CK, Wood WI, Zhang \mathbf{Z}_i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 23; 707pp; English.
                                                                                                                                                                                                                           2000WO-US020710.
2000US-00644848.
2000WO-US023328.
2000US-00664610.
2000US-0065350.
2000WS-00709238.
99WO-USO21090.
99US-00403297.
99US-00423844.
99WO-USO28301.
99WO-USO28551.
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2000US-00747259.
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                                             02-DEC-1999;
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CC PR0917, PR0791, PR01131, PR01116, PR01183, PR01343, PR01760, PR01567 or PR04333), a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PR06029 polypeptide, a method for detecting the presence of tumour in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences cited above. The PRO polypeptide or anti-PRO antibody is useful for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful or substitution probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO colypeptides, in assays to identify other proteins or molecules involved in a binding reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagence if cromosome identification, and transpention to the proposed and nucleic acid molecules are also useful for detecting the presence of a tumour in a mammal, stimulating proliferation or differentiation of chondrocyte cells, stimulating proliferation or differentiation of chondrocyte cells, stimulating colliferation or differentiation of chondrocyte cells, stimulating collurns of the affinity purification of PRO from recombinant cell contact or natural sources. The present sequence is a cDNA encoding a PRO protein 88888888888888888888888888888888888888

Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	1.41e-72	Length:	766
Score:	774.00	Matches:	143
Percent Similarity:	79.07	Conservative:	27
Best Local Similarity:	66.51\$	Mismatches:	43
Query Match:	65.65%	Indels:	7
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US-10-812-620-2 (1-214) x ACA73396 (1-997)

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222	163 caaatgrrcrraridaAcrerridereddaArcecearecraricreagraecridrireare 222	163
40	21 GlnValLeuSerTrpThr1leAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40	2
162	106 ATGAATTCATCTAAATCTGAAACACAATGCACAGAGAGAG	106
20	1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20	-1

223 ACCAGATGTGTGTGACATTTCGCATCTTTCAAACCTGTGAGAAAAAGGTTTCAGCTA 282 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys

TCACAGGAGGAGGAGGAATTCCTTTCCTACAAGAACCTAAAATGAGAGGTTTTTTATT GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 463 140

180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199

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1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
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Human; gene; 88; secreted and transmembrane protein; PRO; TNF-alpha;
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
                  200 SerMetProTrplleCysGluMetProGluIleSerProLeuAsp 214
                           Human secreted/transmembrane protein (PRO) cDNA #12.
                                                       ACA05711 standard; cDNA; 997 BP
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99US-00254311.
99WO-US005028.
99US-00311832.
99WO-US010733.
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99US-00380139.
99US-00380142.
99WO-US020111.
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99US-00403297.
99US-00423844.
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2000WO-US000219.
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99US-00380137.
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18-FEB-2000; 2
22-FEB-2000; 3
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08-NOV-2000;
01-DEC-2000;
                                                                                                                                Homo sapiens.
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01-SEP-1999;
15-SEP-1999;
18-OCT-1999;
12-NOV-1999;
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25-AUG-1999
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transmembrane (PRO) polypeptides. Also disclosed is an antibody that transmembrane (PRO) polypeptides. Also disclosed is an antibody that transmembrane (PRO) polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide, a method for stimulating the cells with a PRO polypeptide, a method for detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the PRO nucleotide sequences. The nucleotide sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoreals purposes, for chromosome identification, as chromosome markers, as therapeutic agents, for stimulating the proliferation or differentiation of chondrocytes and detecting the proliferation or differentiation of chondrocytes and detecting the presence of a tumour. The PRO polypeptides and nucleic acids may also be used disanostically for tissue typing. The sequences
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Wood WI, Zhang Z;
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Matches:
Conservative:
Mismatches:
Indels:
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                      2001US-00816744.
2001US-00854208.
2001US-00854280.
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                                                                                                    2001US-00866028.
2001WO-US017800.
2001US-00874503.
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2001US-00908827.
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2001US-00924419.
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2001WO-US006520
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774.00
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65.65%
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Best Local Similarity:
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                      22-MAR-2001;
10-MAY-2001;
10-MAY-2001;
25-MAY-2001;
01-JUN-2001;
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20-JUN-2001;
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09-JUL-2001;
18-JUL-2001;
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13-AUG-2001;
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Gaps:

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Three hundred and five nucleic acids encoding secreted and transmembrane PRO polypeptides, useful for the diagnosis, prevention and/or treatment of tumors, such as adrenal, lung, colon, breast, prostate, rectal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane). Methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of tumours, such as adrenal, lung, colon, breast, prostate,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-00664610.
2000US-00665350.
2000US-00709238.
                 99US-00380138.
99US-00380139.
99US-0030142.
99WO-US020111.
99US-00403297.
99WS-00433844.
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2000WO-US005841.
2000WO-US006884.
2000WO-US008439.
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2000US-00747259.
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2001US-00854208.
2001US-00854280.
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2001US-00908827.
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                     163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATC 222
                                                                                    100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
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                                                                    ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro
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GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle
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AATTATTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTGAAC 747
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   ThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
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TCCTGGGCGTTAAGTTTAAAGAACTGCTCACCATGGGGGCTCACCTGGTGGTTATCAAC 462
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rectal, cervical or liver tumours. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence represents a cDNA encoding a human PRO polypeptide of the
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Mismatches:

Best Local Similarity:

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New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO335), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
                                                                                                                                                                                                                                                      Ferrara N;
ME, Goddard A;
Kljavin IJ;
                                                                                                                                                                                                                                                                                Tumas D:
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                                                                                                                                                                                                                                                              I, Gerritsen N
Hillan KJ, H
Stewart TA,
                                                                                                                                                                                                                                                       Eaton DL,
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Fong S, Gao W, Gerber H,
Grimaldi JC, Gurney AL, H
an J, Paoni NF, Roy MA, S
                                                                                                                                                                                                                                                                                                                                                                           Example 51; Page 115; 482pp; English.
                                  99WO-US028214.
99WO-US028313.
99WO-US028301.
        99WO-US021090.
99WO-US021547.
99WO-US023089.
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99WO-US020944
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                                                                                                                                                                                                                                                                                                            WPI; 2003-370793/35.
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30-MAR-2000;
22-MAY-2000;
02-JUN-2000;
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Filvaroff E,
Godowski PJ,
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05-JAN-2000;
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Williams PM,
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30-NOV-1999;
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02-DEC-1999;
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16-DEC-1999;
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The invention describes a new isolated nucleic acid molecule comprising
the full length coding sequence of the DNA deposited with the American
type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence
with at least 80% identity to a DNA encoding a PRO polypeptide comprising
any of 61 sequences having 144-1119 amino acids fully defined in the
specification. The PRO polypeptides or polynuclectides are useful as
pharmaccuticals, diagnostics, biosensors or bioreactors. These are
c particularly useful for detecting or treating e.g. Parkinson's disease,
Alzheimer's disease, inflammations, nephritis, wound healing, nerve
cc repair, collateral blood vessel formation, cancers (e.g. colorectal
cancer), haemorrhage (or reduce risk for heamorrhage), rheumatoid
arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
cetenosis, dermal fibrotic conditions (e.g. keloids or scarring),
ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
therapeutic innervention in these diseases, and diagnostic determination
of the presence of these diseases. The PRO polypeptides are also useful
as molecular weight markers, or for chromosome identification. The PRO
consecuted are useful as hybridisation probes, or for screening libraries of
thuman cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
therapy, particularly for replacing a defective gene. This sequence
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27-FEB-2003

997 143 27

Conservative: Length: Matches:

1.41e-72 774.00 79.07%

Percent Similarity:

Alignment Scores

Pred. No.:

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TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC 462
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                                                                                                                                                                                         ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KW Human, PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cliver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy; gene; ss.
                                                                                                                                                                                                                                                     60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys
                                                                                                                                                                                                                                                                     283 CCTGAGAATTTCACAGAGCTCTCCTGCTACAATTATGGATCAGGTTCAGTCAAGAATTGT
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TGTCCATTGAACTGGGAATATTTTCAATCCAGCTGCTACTTCTTTTTTTACTGACACCATT 402
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2233 bp mRNA linear HTC 03-APR-2004
Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
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(calcium dependent, carbohydrate recognition domain) lectin,
superfamily member 9, full insert sequence.
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Baall: GgapDs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
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68 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Haragaki, T., Hara, A., Hashizume, W., Hayaanida, K., Hayatuu, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatuu, M., Hiramoto, K., Hiraoka, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Konno, H., Kagawa, T., Katoh, H., Kawai, J., Kojima, Y., Konno, H., Koda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohasto, N., Okazaki, Y., Saito, H., Saito, H., Sakai, C., Sakai, K., Sakaume, N., Sano, H., Saaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Yakauma, M., Tagawi, M., Tagawa, A., Taya, T., Takaku, T., Tanaki, T., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muranatsu, M. and Hayashizaki, Y. Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission And Hayashizaki, Y. Direct Submission Research Group, RIKEN Genomic Science Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, Nt.: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-922, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-45-503-9222, Fax: 81-
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Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                        The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2233)
                                                                                                                                                                                                                                             The RIKEN Genome Exploration Research Group Phase II Team and the
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GB|NM_019948, evidence: BLASTN, 99%, match=1386)"
                                                                                                                                                                                                                                                                        FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                         / sex="female, virgin" | tissue_type="infiltrating ductal carcinoma" | tissue_type="infiltrating ductal carcinoma" | tissue_type="infiltrating ductal carcinoma" | lab_host="DH10B" | lab_host="bH10B" | lab_host="lab="NOI CGAP_Mam6" | note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: NoI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 ProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeuThr 100
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomica, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.lnl.gov.row: g column: 24 Plate: LLAN7650 row: g column: 24 High quality sequence gtop: 625.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas BY743963 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone 1830025C13 5', mRNA sequence. Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226 Email: genome-reseggec.riken.jp, URL:http://genome.gsc.riken.jp/
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Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,P.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojims,Y.,
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Direct Submission Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1. (bases 1 to 717) Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format

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On Jan 26, 2001 this sequence version replaced gi:12562986.

Other ESTS: H3053008-3

Contact: George J. Kargul
Laboratory of Genetics

National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov

This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3053 row: D column: 08
Seq primer: -21M13 Reverse
H4Gh quality sequence stop: 644
POLYA=NO.
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Genome-wide expression profilling of mid-gestation placenta and embryo using a 15,000 mouse development of DNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97:9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3)
Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7:5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
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Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H. III, Becker, K.G. and Ko, M.S.H. Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-rime sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (201)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Genom in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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| Arzain="CSPL/64" |
| Arzain="CSPL/64" |
| Ab xref="taxon:1000" |
| Clone="1830025C13" |
| Arisaue_type="hone marrow" |
| Cell_type="macrophage" |
| Clone_lib="RIKEN full-length enriched, bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tgurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226 Fax: 81-45-503-9226 Email: genome-reseges riken.jp, URL:http://genome.gsc.riken.jp/Adachi.jc, Aizawa.K., Akimura.T., Arakawa.T., Carninci.P., Rukda.S., Hashizume, W., Hayashida.K., Hirozane.T., Hori.F., Imotani.K., Ishii.Y., Itoh, M., Kagawa.I., Kawai.J., Kojima.Y., Kondo.S., Konno.H., Koya.S., Miyazaki.A., Murata.M., Nakamura.M., Nomura.K., Numazaki.R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sanc, H., Sasaki.D., Sato, K., Shibata.K., Shiraki.T., Tagami.M., Takeda, Y., Waki.K., Watahiki.A., Muramatsu.M., and Hayashizaki.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subbraction of cap-trapper-seelected cDNAs to prepare full-length cDNA libraries for trapper seelected cDNAs to prepare full-length cDNA libraries for trapper seelected cDNAs to prepare Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome .
Encyclopedia Project of Genome Exploration Research Genome in Riken Genomic Science and Genome Science Laboratory in Riken Genomic Science Conter and Genome Science Laboratory in Riken prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust (MRC building Addenbrookes Hospital Cambridge) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, NOD-derived CD11c
+ve dendritic cells"
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/strain="NOD"
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E. 1 (bases I to 667)
S. Acazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yadi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Batsel, K., W., Blake, J. A., Bradt, D., Brusic, V.
Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C. P., Forrest, A., Frazer, K.S., Gaasterland, T.,
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Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
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BY747840 RIKEN full-length enriched, NOD-derived CD11c +ve
dendritic cells Mus musculus CDNA clone F630012G18 5', mRNA
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Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiranco, K., Hiraoka, T., Hirozane, T., Hayashi, T., Inciani, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kayas, T., Miyazaki, M., Muraara, T., Miyazaki, M., Muraara, M., Mushi, K., Nomura, T., Miyazaki, R., Ohno, M., Ohaato, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Subiraki, T., Tagawi, M., Tagawa, A., Takahaahi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission

L. Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN). Laboratory for Genome Exploration Research Group, RIKEN Genome Center (GSC), Kanagawa 210-0045, Japan (E-mail:genome-resegge: riken:jp, NRL: Http://genome-gsc.riken:jp, NR
                                      Vonno, H., Akiyama, J., Najawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanmancto, R., Natsumcto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKAN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer 2053033
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/clone lib=RIKEN full-length enriched mouse cDNA library"
/dev stage="adult"
1. .4017
/fore="C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (MGD|MGI:1861232, GB|NM_019948, evidence: BLASTN, 99%, match=1386)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
6 60,70 &1011-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4017)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse cDNA collection
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Location/Qualifiers
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/strain="C57BL/6J"
/d_xref="FANTOM DB:9830118H07"
/db xref="taxon:10090"
/clone="9830118H07"
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Mus musculus adult male bone cDNA, RIKEN Full-length enriched library, clone:9830118H07 product:C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9, full
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        TrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValVal1leAspThr 120

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnGluGluGlnGluPheleuPheArgThrLysProLysArgLysGluPheTyrIleGly 140
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
Mus musculus (house mouse)
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94.39%
80.11%
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Schonbach, Y., Yogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
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BY744630
BY744630.1 GI:27171386
                                                                                                                                                                                                                                                                                                                                                                        TyrSerGluAlaSerGlySerValLyaAanCyaCyaProLeuAanTrpLyaHiaTyrGln
                                                                                                                                                                                                                                     --CyBValValThrTyrArg
                                                                                                                                                                                                                                                                      2584 AGCACTGAAAAGGACACAAAGCATTAACCACTTCCCTTTCCTCTTACAGTAACATATCGC
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Mus musculus
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Frecher, C. Corbani, L. Cousies, S. Dalla B. Dregen, T.A.,

Frecher, C. F., Forrest A., Frezer, K.S., Casterind, S.,

Garibodi, W. Gissic, C., Goddi, M., Godgi, J. Girmand, S.,

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Waller, M., Milling, L.G., Wyndhavs, B.C., Setou, M., Shimada, K.,

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Sakazuse, M., Sato, K., Shiraki, T., Waki, K., Mang, Y., Watanba, K.,

Sakazuse, M., Sato, K., Shiraki, T., Waki, K., Mang, J., Mander, E.S.,

Sakazuse, M., Sato, K., Shiraki, T., Waki, K., Mang, J., Mander, E.S.,

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Sakazuse, W., Sato, K., Shiraki, T., Waki, K., Mang, J., Mang, J.,

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Sakazuse, M., Sato, K., Mayazi, A., Azaka, K., Sasaki, D., Shinae, K.,

Sakazuse, M., Sato, K., Mang, M., Anderia, M., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D., Sasaki, D.,
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SM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 655)

S (Azaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,

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Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.M., Majott, D.R., Maltais, L., Marchionni, L., McKenzis, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Ralg, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takranak, Y., Taylor, M.S., Tasdala, K.D., Tonita, M., Verardo, R., Wanner, A., Yang, I., Wanner, A., Zarninabe, Y., Wanger, L., Wahnestedt, C., Wang, Y., Warnabe, Y., Wanger, L., Wahnestedt, C., Wang, Y., Warnabe, Y., Wang, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yang, L., Xang, L., Xang, L., Xang, L., Xang, L., Xang, L., Kana, Y., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Sakazume, N., Hara, A., Hashizume, W., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Miyazaki, J., Sakai, Waterston, R., Lander, E.S., Shinagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, I., Miyazaki, A., Sakai, Y., Materston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-langth cDNa
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
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Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M., and Haysshizaki,Y.
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/clone_lib="RIKEN full-length enriched, NOD-derived CD11c
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Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
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Ravasi,T., Reed,J.C., Redd,D.J., Ring,B.Z.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
Verardo,K., Wagner,L., Wahlestedt,C., Wang,Y., Watenabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zhmmer,A., Carnind,P.,
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Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Pukuda,S., Hara,A., Hashizume,W., Imoteni,K.,
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Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length, Conna
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Email: genome-res@gec.riken.jp, URL:http://genome.gec.riken.jp/.
Adachi.J. Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashidaa,K., Hizozane,T., Horl.fe.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojina,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohlo,M., Shitch,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramateu,M., and Hayashizaki,Y.
Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequence Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Genomic Science Tissues

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details
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The Institute of Physical and Chemical Research (RIKEN)
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Genoup in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavodan, M., Zhu, Y., Zimmer, A., Garnind, P., Savodan, M., Zhu, Y., Zimmer, A., Garnind, P., Sakazume, N., Hirozane-Kishikawa, T., Komo, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imctani, K., Ishii, Y., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashiraki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cobnsc
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Muses I (bases I to 728)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 ACCAGATGTGTGTAACATATCGCAGCTCTCAAATTTCCGGGCAGAACTTACAGCCACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 CCTTIGAACHGGAAACATTATCAATCTAGTTGTTATTTTTTCTCTACGACAACCTTGACC
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retrovaky, N., Pillai, R., Pontius, J.U., Oi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, J.C., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Taklor, M.S., Taesdale, R.D., Tomita, M., Verardo, R., Wagner, L., Waheletedt, C., Wang, Y., Watanabe, Y., Walls, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yana, J.Z., Zavolan, M., Zhimer, A., Carninci, P., Haydeteu, M., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Ishi, I.Ch, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Birney, B. and Hayashizaki, Y. Rogers, J., Birney, B. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Genomic Sciences Center and Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Day Institute for Molecular Bloscience
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
11-7-22 Suchikro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9216
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| Biriain="CSPIL/6J"
| db xref="taxon:10090"
| clone="1830011F16"
| clissue type="bone marrow"
| cell type="marrophage"
| clone_lib="RIKEN full-length enriched, bone marrow
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Pred. No.:
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S. Acazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaqi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Golobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Ouackenbush, J., Schriml, L.M., Kanapin, A., Masuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Jarvis, E.D., Kanagi, A., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lenhard, B., Lyone, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKanzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
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                                                                                   TrpSerSerSerLeuLygAsnCygSerAspMetGlyAlaHisLeuValVallleAspThr 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu 160
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musculus cDNA clone 1830011F16 5', πRNA sequence.
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walla, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Garninci, P., Hayatsu, N., Hirozanae-Kishikawa, T., Konno, H., Nakamura, M., Zixakawa, T., Kanai, J., Yazawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, J., Myazaki, A., Yashino, W., Materston, K., Lander, E.S., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60, 770 full-length conns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-reseggec.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itch,M., Kagawa,I., Kwai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Satto,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/organism="Mus musculus"
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S. Adazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Yamanaka, I., Kiyosawa, H., Yadi, K., Tomaru, Y., Hasagawa, Y., Nogami, A., Schonbach, C., Golobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batael, K. W., Blake, J.A., Brade, J.A., Brade, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garibnoidi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedziereki, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Nurcchkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Percysky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ringwald, M., Sannedin, A., Schneider, C., Semple, C.A., Serou, M., Shinada, K., Sultana, R., Takloraka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
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musculus cDNA clone I830018A02 5', mRNA sequence.
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Unject summission, Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new SIREN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Muuse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Center for Molecular Mechanisms in Disease Wellcome Trust Center for Molecular Mechanisms in Disease wellcome assistance we gratefully acknowledge: visit our web site (http://genome.gsc.riken.go.jp) for further details
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, W., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizo, M., Waterston, R., Lander, E.S., Analysis of Ethe mouse transcriptome based on functional annotation of 60, 770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
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Adachi,J., Aizwa,K., Akimura,T., Arakawa,T., Carninci,P.,
Rukuda,S., Hashiatume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kwaii,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M., and Hayashizaki,Y.
Direct Submission
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+ve dendritic cells"
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/clone="F730001C01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yoshihide Hayashizaki
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Sokazaki, Y. Furuno, M. Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikalado, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyoswa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasaterland, T., Gustinoich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurokhin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachadran, S., Ravasi, T., Reed, J.C., Semple, C.A., Setou, M., Shimada, K., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R.D., Tomita, M., Verardo, R., Walles, C., Wilming, L.G., Whinhaw Edoris, A., Yanagisawa, M., Yang, I., Yang, I., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Vangile, P., Kang, I., P., Kang, I., Konno, H., Nakamura, M.,
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                                                                                                                                                                                                                                                                                                                         184 CAAGTGCTCTCCTGGACGATAGCCGGGCCTCCATCTTCTTCAGTGGCTGTTTCATC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProLeuAanTrpLysHiaTyrGlnSerSerCysTyrPhePheSerThrThrThrLeuThr 100
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Loformiaes 1 to 671)
                                                                                                                                                                                                                                                                             GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCyaPheIle 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ArgAsn11eLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCysCys
                                                                                            MetabnSerThrLygSerProAlaSerHisHhrGluArgGlyCysPheLygAsnSer
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486 bp mRNA linear EST 27-JUN-2003
BK516799 NCI CGAP Mam6 Mus musculus cDNA clone IMAGp998G247650 ;
INAGE:3158063, mRNA sequence.
/note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2: BCoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/AnoI sites using the following 5' adaptor: GGCAGGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
                                                                                                                                                                                                                                                                                                       ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyalaHisLeuValVallleAsp 119
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Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.inih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM186 row: g column: 08
High quality sequence start: 24
High quality sequence start: 24
High quality sequence start: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                  602
                                                                                               244 ACCAGATGTGTCGTAACATACGCTGCTCTCAAATTTCCGGGCAGAACTTACAGCCACAT 303
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1032)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                           61 ArgAsnIleLysGluLeuSerCysTyrSerGluAlaSer-------
                                                                                                                                                                                                                                                               484 ACAACCTTGACCTGGTCATCAAG-TTAAAGAATTGCTCAGACATGGGGGGCTCACCTGGTG
                                                                              ThrArgCysValValThrTyrArgSerSerGlnIleSerGlnAgnAsnLeuGlnProHis
                                                                                                                                                            97 ThrThrLeuThrTrpSerSerSerLeuLy8AsnCy8SerAspMetGlyAlaHisLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                  543 GTTATCGACACACAGGAAGAGCAGGAATTCCTTTTTCGCACAAAACCTAANAGGAAAGG
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364 CAGAATCATTAGCAAAGTTTCTGGGCAATGTCTGAAGCCTTTCTCCTCTTAGGTTCAGTC
                                                                                                                                                                                                     74 ---------GlySerVal
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BE311916.1 GI:9148643
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                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 486)
Hell,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D. and Korn,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 ATGAATTCAACCAAATCGCCTGCATCCCACACACAGAGAGGATGCTTCAAAAACTCC 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnValLeuSerTrpThr1leAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheile 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free from RZPD; conteact RZPD (chone@rzpd.de) for further information. Seq primer: SP6, Primer sequence: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer
                                                                                                                                                                                           Mouse Uniqueset - RZPD2
Unpublished (2003)
Contact: Ina Rolfs
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD, INAGP998G247650.
RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
RAZPLIB; I.M.A.G.E. CDNA Clone Collection;
Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
http://www.rzpd.de/CloneCards/Cgi-
bin/showLib.pl.cgi/response7libNo-981 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 111
www.rzpd.de
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    .486
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